

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 121508

TO: Jennifer Graser

Location: rem/3b09/3c18

Art Unit: 1645

Monday, May 10, 2004

Case Serial Number: 10/625221

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Graser,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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GenCore version 5.1.6
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OM protein - protein search, using sw model

May Run on:

7, 2004, 12:05:23 ; Search time 21 Seconds (without alignments) 1012.301 Million cell updates/sec

US-10-625-221-14 1178 1 QODPDPSQLHRSSLVKNLQN......KDNETLDSNTSQIEVXLTTK 221 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

123 10.4 227 2 C89808 Experiments 114 9.7 292 2 B89807 Experiming 12.5 9.6 234 2 C89807 Experiming 9 [90.5 9.3 1367 2 T124466 hypothetical 05.5 9.0 232 2 F89807 Experiming	0.1444080000046800000440000444	OM 1	Length Le	ш наааннаанаааааааааааа	1D 529659 518786 518786 518789 5218786 511885 5	10.0.0.d d d d d d
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FUSION, methionine hypothetical prote	immunoglobulin Al	toxic shock syndro	desmocollin 1b pre	desmocollin la pre	Dscla precursor -	Dsclb precursor -	hypothetical prote	toxic shock syndro	hypothetical prote	hypothetical prote	hypothetical prote	prrC protein - Esc	ë	ORF MSV152 probabl
E96935	800860	XCSAS1	B48910	A48910	137281	137282	T18489	B89992	G90604	D95019	B8988	809627	C70168	T28313
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596 208	1856	234	770	824	840	894	4981	234	493	463	241	396	908	1306
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105.5	102	101	101	101	101	101	100	86	8	97.5	96	96	96	96
30	3 7	33	34	35	36	37	38	9	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12 Nighternate names: erythrogenic toxin; erarlet fever toxin
	C;Species: streptococcus progents prage 11. C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999 C;Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800 R;Weeks, C.R.; Ferretti, J.J.
	Infect. Immun. 52, 144-150, 1986 A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g A;Reference number: S29659; MUID:86166804; PMID:3514452 A;Accession: S29659
	A;Molecule type: DNA A;Residues: 1-251 «WED» A;Cross-references: GB:U40453; EMBL:M19350; NID:g1877426; PIDN:AAC48868.1; PID:g1877430 R:Nelson, K.: Schlievert, P.M.; Selander, R.K.; Musser, J.M.
	J. Exp. Med. 174, 1271-1274, 1991 A; Itle: Characterization and clonal distribution of four alleles of the speA gene encocharge number: S18782; MUID:92044323; PMID:1940804
	A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
	A;Kestoues; 9-244 KNEL. A;Cross-references: BMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288 A;Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
_	Astrocesing signal acid sequence not shown; translation not shown A; Molecule type; DNA.
	A;KeBindues; 9-244 KNEAP, ANEAP, A;KeBSG6; NID:g47291; PIDN:CAA43754.1; PID:g47292 A;Cross-references: EMBL:X61556; NID:g47291; A;Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigne A;Note: the nucleocide sequence was submitted to the EMBL Data Library, September 1991 A:Arression: G1978
	A. A. Status: nucleic acid sequence not shown; translation not shown A. Molecule type: NURA A. NURA A. NURA AND A.
	Archsiumes: 7-247 ANEL: MNEL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294 A; Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned pla; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
	Afficession: S107)1 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A:Desidence: 9-244 ANYY.
	A;Cross_references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310 A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned A;Note: the nucleocitie sequence was submitted to the EMBL Data Library, September 1991 A;Accession, C14706
	A; Accession: Signature acid sequence not shown; translation not shown A; Status: nucleic acid sequence not shown; A; Molecule type: DNA A; Residues; 9-24 A NEO-34 A
-	P.(LOGG'LELECTO)

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excitoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isoli N;Alternate names: scarlet fever toxin (5;Species: Streptococcus pyogenes phages had alled the california; strain MGAS250 isolate Garmany (5,Date: 29-Jan.1993 #sequence revision 29-Jan.1993 #text change 16-Jul.1999 (5,Date: 29-Jul.1999 (5,Date: 29-Jul.1999) (5,Date: 29-Jul.1999 (5,Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
A;Experimental source: strain MGA8624 isolate Germany unassigned phage
A;Notes: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Experimental source: strain MGAS250 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: strain MGAS251 isolate California unassignd phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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      A, Residues: 1-236 <NEZ>
A, Rossidues: references: EMBL:K61570; NID:g47315; PIDN:CAA43768.1; PID:g47316
A, Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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C;Genetics:
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A; Residues: 1-236 <NEL>
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A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassig
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
      -14
Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991; Accession: S18797
                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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                                                                                                                                                             A,Status; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
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Pred. No. 4e-83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.5%;
Matches 220; Conservative C
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C,Superfamily: enterotoxin B
C,Keywords: exotoxin n
F;1-30/Domain: signal sequenc
F;31-251/Product: exotoxin ty
                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 9-244 <NEH>
A,Cross-references: PMRT
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exceptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
NyAlternate names: scarlet fever toxin; SPE type A (speA)
NyAlternate names: scarlet fever toxin; SPE type A (speA)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26152
Michael A26152
Michael Gent. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta A;Accession: A26152
A;Molecule type: DNA
A;Accession: A26152
A;Molecule type: DNA
A;Mesides: 1-250 c/OH>
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
            encod
A;Title: Characterization and clonal distribution of four alleles of the speA gene encon A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Reference number: S18789
A;Rotatus: nucleid acid sequence not shown; translation not shown
A;Rotatus: nucleid acid sequence not shown; translation not shown
A;Residues: L-236 <NEL>
A;Residues: L-236 <NEL
A;R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 DGIQSLSFDIEQIKN-GNCSRISYTVRKYLIDDNKQLYINGPSKKETGYIKFIPKNKESFW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 NQEMATLFKDKOVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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                                                                                                                                                                                                                                                                                                                                                                                                   C,Superfamily: enterotoxin B
S,Reywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
87.0%; Score 1025; DB 2; Length 23
Best Local Similarity 89.7%; Pred. No. 4.9e-72;
Matches 192; Conservative 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 TFWPDFFPEPEFNQVKYLMIYKDNETLDSSTSQI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch
(al Similarity 86.7%; Pred. No. 2.1e-68;
189; Conservative 4; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 189
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A,Gross-references: EMBL.X61564; NID:947305; PIDN:CAA43762.1; PID:947306
A,Rocestion: 1-236 cNEY-
A,Gross-references: EMBL.X61564; NID:947305; PIDN:CAA43762.1; PID:947306
A,Rocestion: 1818792
A,Status: nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Rocession: 1236 cMBL.X61565; NID:947311; PIDN:CAA43763.1; PID:947312
A,Rocession: 818795
A,Roces
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A/Cross-references: EMBL:X61563, NID:947301, PIDN:CAA43761.1; PID:947302
A/Experimental source: strain MGAS256 isolate California unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18790
A/Accession: S18790
A/Accession: S18790
A/Accession: S18790
A/Accession: S18790
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                                    Status: nucleic acid sequence not shown; translation not shown Molecule type: DNA
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                        A;Accession: S18788
A;Status: nucleic ac
A;Molecule type: DNA
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A, Accession: A60114
A, Status: not compared with conceptual translation
A, Status: not compared with conceptual translation
A, Status: not compared with conceptual translation
A, Status: 1.266 - EBDH>
A, Racession: B60114
A, Molecule type: Drottein
A, Racession: B6014
A, Molecule type: As - EBCHP>
A, Accession: B6014
A, Molecule type: As - EBCHP>
A, Molecule type: As - EBCHP>
A, Accession: B6014
A, Molecule type: As - EBCHP>
A, Accession: A33866, MulD:89327174; PMID:2473979
A, Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests the A, Reference number: A33866, MulD:89327174; PMID:2473979
C;Species: Staphylococcus aurens
C;Species: Staphylococcus aurens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 12.04 #1990
A;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
A;Hother Canada and Canada 
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N;Alternate names: enterotoxin C-3 precursor
C;Species: Staphylococcus aureus
C;Date: 10-Nov-1992 #sequence revision 10-Nov-1992 #text_change 16-Jul-1999
C;Accession: A60114; B60114; Ā33866
C;Accession: A60114; B60114; Ā33866
C;Accession: A60114; B60114; Ā33866
A;Bohach, GA.; Schlievertr, P.N.
Infect. Immun. 57, 2249-2252, 1989
A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins A;Reference number: A60114; MUID:89277549; PMID:2543637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 LEIP--KKIVVKVSIDGIQSLSFDIBTNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
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A;Molecule type: DNA
Asesidues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
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F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

46.3%; Score 546; DB 2; L
Best Local Similarity 47.2%; Pred. No. 5.7e-35;
Matches 111; Conservative 43; Mismatches 67;
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Pred. No. 9.8e-35;
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Best Local Similarity
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                                      Cipecies: Stabhylococcus aureus
Cipacies: 24-Apr-1994 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
Cipacession: S27360; A92065; $27240; A01815
Cipacession: S27360; A92065; $27240; A01815
Cipacession: S27360; A92065; $27240; A01815
J. Bacteriol. 166, 29-33, 1986
A;Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A;Reference number: S27360; MUD: 86168029; PMID: 3957869
A;Residues: 1-266 < JONA
A;Residues: 1-266 < JONA
A;Residues: 1-266 < JONA
A;Cocss-references: EMBL:M1118; NID: 9152999; PIDN: AAA88550.1; PID: 9153000
A;Experimental source: strain 86
B;Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A;Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromid A;Reference number: A92065; MUID: 71007902; PMID: 5470821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 KLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLCENA------BRSACIYGGVTNHE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGP---NYD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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48.6%; Score 572; DB 1; Length 266;
Best Local Similarity 49.2%; Pred. No. 5.6e-37;
Matches 116; Conservative 36; Mismatches 68; Indels
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu, K.;
C;Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Recession: A89969
A;Accession: A89969
A;Accession: A89969
A;Accession: A89969
A;Accession: C;Accession: A89969
A;Accession: A89699
A;Accession: A89969
A;Accession: A89699
A;Accession: A8969
A;Accession: A89699
A;Acce Cyaccession: G89568
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C; Skimizu, F.; A; Mizurani-ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Rocession: G89968
A; Accession: G89968
A; Accession: G89968
A; Residues: 1-258 ckUR>
A; Residues: 1-258 ckUR>
A; Cross-references: GB:BA000018; FID:g13701617; FIDN:BAB42910.1; GSPDB:GN00149
A; Experimental source: strain N315 ά, 149 VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPE--PEFTQSKYLMIYKDNET 206 121 110 111 LEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETG 170 61 85 95 RSACIYGGVTNHEGNHL-----EIPKKIVVKVSIDGIQSLSFDIETNKKWVTAQELDYK 62 VRNYLLKHKNLYEFNSSPYETGYIKFIEGSGHSFWYDLMPESGKKFYPTKYLLIYNDNKT 57 KLKTELKNOEMATLFKOKNVDIYGVEYYHLCYLCENAE-----RSACIYGGVTNHEGNH 86 EVKTELENTELANNYKDKKVDIFGVPYFYTCIIPKSEPDINQNFGGCCXYGGLTFNSSEN 146 -ERDKLÍTVOVTIDNRÓSLGFTÍTÍNKNÁVTIÓELDÝKARHWLÍKEKKLYEFDGSAFESG 1 QODPDPSQLHRSSLVKN----LONIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYD 26 QPDPKLDELNKVSDYKGNNKGTMGNVMNLYTSPPVEGRGVINSRQFLSHDLIFPIEYKSYN 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 B; Gaps 171 YIKFIPKNKESFWFDFFPEPE---FTQSKYLMIYKDNETLDSNTSQIEVYLTT 205 YIKFTEKNNTSFWFDLFPKKELVPFVPYKFLNIYGDNKVVDSKSIRKEVFLNT enterotoxin_YENT2_[imported] - Staphylococcus aureus (strain N315) Length 136; 39.7%; Score 468; DB 2; Length 258; 43.8%; Pred. No. 5.8e-29; active 39; Mismatches 78; Indels Query Match
28.6%; Score 337; DB 2; Length 130
Best Local Similarity 49.6%; Pred. No. 3.4e-19;
Matches 67; Conservative 22; Mismatches 38; Indels 207 LDSNTSQIEVYLTTK 221 Query Match
Best Local Similarity 43.8[†]
Matches 102; Conservative C,Genetics: A,Gene: seg C,Superfamily: enterotoxin B A; Gene: yent2 g ò 음 8 ģ 엄 $\dot{\delta}$ d ò 용 장 g à ENSACT
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C; Species: Staphylococcus aureus
C; Species: Staphylococcus
C; Accession: S06356, A01816
R; Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A; Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness the status sofisson MUD: 88038352; PMID: 2823067
A; Accession: S06356
A; Molecule type: DNA
A; Residues: 1-266 <BOH>
A; Cross-references: EMBL: X05815; NID: 946566; PIDN: CAA29260.1; PID: 946567
A; Cross-references: EMBL: X05815; NID: 946566; PIDN: CAA29260.1; PID: 946567
A; Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A; Reference number: A01816; MUID: 83213327; PMID: 6189824
A; Accession: A01816
A; Molecule type: Protein
A; Residues: 28-75, 'IL', 78-176,'N', 178-266 <SCH>
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Csuperfamily: enterotoxin B
C; Keywords: enterotoxin signal sequence #status experimental <AA7>
F; 28-266 / Product: enterotoxin C-1 #status experimental
F; 120-137 / Disulfide bonds: #status experimental ž G89968 extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain C;Species: Staphylococcus aureus PDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE 209 57 KLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGNH 110 111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYF 168 ŝ 168 150 FDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE 209 1 QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSG---PNYD 56 89 57 KLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGNH 110 8 26 30 QPDPTPDELHKASKFTGLMENMKVLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD 30 QPDPTPDELHKSSEFTGTWGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNYD 111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 1 QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSG---PNYD TGYIKFIPKUKESFWFDFFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221 Gaps TGYIKFIPKNKESFWFPFFFFF--FFTQSKYLMIYKDNETLDSNTSQIBVYLTTK 221 14; 14; Query Match
Best Local Similarity 46.8%; Pred. No. 1.2e-34;
Matches 110; Conservative 44; Mismatches 67; Indels Indels 67; Mismatches

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enterotoxin C-1 F

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C;Species: Staphylococous aurous
C;Species: Staphylococous aurous
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 11: Baba, T:; Yuzawa, H:; Kobayashi, I:; Ogucl
R;Kuroda, M:; Ohta, T:; Wobayashi, N:; Sawano, T:; Inoue, R:; Kaito, C:; Sekimizu, K:; Inoue, B.; Mattori, M:; Gasawara, N:; Hayashi, H:; Hiramatsu, K.
Innote 357 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89968
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cispecies: Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accesion: C99894
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Cross-references: GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-260 «KUR»
A;Cross-references: GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 NQEMATLFKDKNVDIYGVEYYHLCYLCENAE--RSACIYGGVTNHEGNHLEIPKKIVVKV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 SIDGIQSL--SFDIETNKKAVTAQELDYKVRKYLTDNKQLYT----NGPSKYETGYIKFI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 WIDGKQNTVPLGTVKTNKKEVTVQELDLQSRHYLHETYNLYNTDAFNG--KIQRGLIEFH 214
99
                                                                                                                     NHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYN--VSGPN-YDKLKTELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                  207 KGYIKFHSHSEHKESFYYDLFYIKGNLPDQYLQIYNDNKTIDSSDYHIDVYLFT
                                                                                                                                                                                                                                                                                TGYIKE -- IPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
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26.8%; Score 315.5; DB 2;
Best Local Similarity 36.7%; Pred. No. 3.6e-17;
Matches 84; Conservative 44; Mismatches 74;
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C,Superfamily: enterotoxin B
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A;Status: preliminary
A;Molecule type: DNA
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B89969

enterotoxin SeO (imported) - Staphylococcus aureus (strain N315)

C)Species: Staphylococcus aureus

C)Bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C)Accession: B89969

R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Reference number: A89758; PMID:11418146

A;Reference number: A89758; PMID:11
                                                                                                                                                                                                                                                                                    C;Species: Staphylococcus aureus
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C;Dates: 03-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
B;Bayles, K.W.; Iandolo, J.J.
J; Bayles, K.W.; Iandolo, J.J.
J; Bacteriol. 171, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin A;Reference number: A33953; MUID:89359112; PMID:2549000
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 NIMINGVQKEVSLDKVQTDKKAVITVQELDAQARRYLQKDLKLYNNDTLGGKIQRGKIEFD 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 INFNSKEMAQHFKSKNVDVYPIRYSINCYGGE-IDRTACTYGGVTPHEGNKLKERKKIPI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVSIDGIQ-SLSFD-IETNKKM/TAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QODPDPSQLHRSSLVK--NLONIYFLYEGDPVTHENVKSV----DQLLSHHLIYN----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 OLHR-----SSLVKWLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYN---VSGPNYDKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA,
XResidues: 1-238 - CABA.
A;Cross-references: GB:MZ8521; NID:91492109; PIDN:AAB06195.1; PID:9758691
C;Superfamily: enterotoxin B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.3%; Score 333.5; DB 2; Length 258; 36.7%; Pred. No. 1.4e-18; tive 42; Mismatches 86; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLYEK 258
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27.5%; Score 323.5; DB 2
Best Local Similarity 38.5%; Pred. No. 8.6e-18;
Matches 90; Conservative 33; Mismatches 94
                                                                                                                                                                                                                                                   enterotoxin D precursor - Staphylococcus aureus
                122 VESKSINVEVHLTKK 136
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Query Match
25.3%; Score 297.5; DB 2; Length 258;
Best Local Similarity 35.8%; Pred. No. 8.6e-16;
Matches 77; Conservative 39; Mismatches 86; Indels 13; Gaps C,Genetics: A,Gene: sen C,Superfamily: enterotoxin B

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Search completed: May 7, 2004, 12:09:40 Job time: 22 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

May 7, 2004, 12:01:27; Search time 17 Seconds (without alignments) 676.912 Million cell updates/sec US-10-625-221-14 1178 1 QODPDPSQLHRSSLVKNLQN......KDNETLDSNTSQIEVYLTTK 221 Title: Perfect score: Sequence:

141681 seqs, 52070155 residues Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STEMMEN

		Description	08095	P01552 staphylococ		P34071 staphylococ				P13163 staphylococ	P12993 staphylococ							escherich					Q03529 saccharomyc	Q04956 plasmodium	P89876 1 genome po	Q9zd66 rickettsia	Q8cp23 staphylococ		clostridi	₩.				19995 clostridi	Q01206 barley yell
SUMMARIES				ETXB_STAAU	ETC3 STAAM	ETC2_STAAU	ETC1_STAAU	ETXG_STAAM	ETXD_STAAU	ETXA_STAAW	ETXE_STAAU	ETXH_STAAW	SPEH STRPY	SPEC STRPY	SPEG_STRPY	TSST_STAAU	DSC1_HUMAN	PRRC_ECOLI	DPO1_BORBU	HGP2 HAEIN	PURA_WIGBR	PRIA_BORBU	SCS7_YEAST	ATX1_PLAFA	POLG_LMVE	Y478_RICPR	PRIM_STAEP	POLG LMV0	NADB_CLOPE	RNE_BUCAP	Y243 AQUAE	MTA1 ACICA	RM06_ACACA		POL1_BAYMJ
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P49048 caenorhabdi Q91t47 arabidopsis	Q8czeł oceanobacil P26450 mus musculu	049409 mycoplasma	P47084 Baccharomyc	Q8dvs2 streptococc	Q01107 bos taurus	Q9kiv0 haemophilus	P33459 caprine art	Q04574 barley yell
GPI8 CAEEL FIE ARATH	MUEZ_OCEIH	Y277_MYCGE	YJX3 YEAST	PEPX_STRMU	DSC1_BOVIN	HGBC HAEIN	POL_CAEVC	POLI_BAYMG
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Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Crystal structure of staphylococcal enterotoxin B, a superantigen.";
Nature 359:801-806(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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                                                                                                                                                                                                                                                                                                                                                                          31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKKK
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MEDILINE-7100902, PubMed=5470821;
MEDILINE-7100902, PubMed=5410821;
Withen I.-Y., Bergdoll M.S.
"The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";
B, and the complete amino acid sequence.";
J. Biol. Chem. 245:3518-3525(1970).
                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE=85298255; PubMed=3898073;
Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
"Molecular cloning of staphylococcal enterotoxin B gene in
"Becherichia coli and Staphylococcus aureus.";
Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854 (1985).
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                                                                                                                                                                                                                          Length 251;
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                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                           29246 MW; 54001FE4CCCBFCC3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                                                                                          Score 1169; DB 1;
Pred. No. 2.4e-82;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 166:29-33(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterotoxin type B precursor ENTB.
                                                                                                                                                                                                                             99.2%;
ilarity 99.5%;
Conservative C
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             chain.
MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQEVPAQQDPD -> LPKGICSTRPK (IN REF. H -> Q (IN REF. 2).
S -> N (IN REF. 2).
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I -> L (IN REF. 2).
TNKKMVTAQELDYK -> QIKNGNCSRISYT (IN
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S -> N (IN REF. 2).
NLQNIYFLYEGDP -> TFKIYIFFMRVTL
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PDB; 1B1Z; 24-NOV-99.
PDB; 1B1Z; 24-NOV-90.
PDB; 1FNV; 17-NOV-00.
PDB; 1FNV; 17-NOV-00.
PDB; 1FNV; 17-NOV-00.
PDB; 1LOX; 03-APR-02.
InterPro; 1PR006192; Bact endotox.
InterPro; 1PR006192; Bact endotox.
InterPro; 1PR006133; Stap/Strep_toxin.
InterPro; 1PR006133; Stap/Strep_toxin.
InterPro; 1PR006133; Stap/Strep_toxin.
InterPro; 1PR006135; Stap/Strep_toxin.
InterPro; 1PR006135; Stap_Strp_tox Of: 1
PEam; PF02876; Stap_Strp_tox Of: 1
PRNINTS; PR00279; BACTRATOXIN 1; PROSITE; PR00279; STAPH_STREP_TOXIN 1; IPROXIN; Signal; 3D-Strp_CoxIn 2; IPROXIN 3; STAPH_STREP_TOXIN 2; IPROXIN; Signal; 3D-Strp_CoxIn 3; IPROXIN 3; IPROXIN; Signal; 3D-Strp_CoxIn 3; IPROXIN; Signal; 3D-Strp_CoxIn 3; IPROXIN; IPROXIN; IPROXIN; Signal; 3D-Strp_CoxIn 3; IPROXIN; IPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN REF. 2)
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VT -> MK (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXOTOXIN TYPE A.
                                                                                                                                                                                                                                                                                                                                                                                                 , AE009982; AAL97141.1; -. A26152; A26152.
                                                                                                                                                                                                                                                                                                                                                    EMBL; U40453; AAC48868.1; -. EMBL; X03929; CAA27568.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
                                                                                            X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR. MEDLINE=99905298; PubMed=981971; Li H., Libra A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M., Karjalainen K., Mariuzza R.A.; "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B."; Immunity 9:807-816(1998).
                                                                                                                                                                                                                                                                                                                                                        X-73 CRYSTALLOGRAPHY (1.5 ANGSTROMS).
MEDLINE=98181012; PubMed=9514739;
Papageorgiou A.C., Tranter H.S., Acharya X.R.;

Ecognition B. L.S.A resolution: implications for superantigen
recognition by MHC class II molecules and T-cell receptors.";
J. Mol. Biol. 277:61-79(1998).
J. Mol. Biol. 277:61-79(1998).
Staphylococcal enterotoxins cause the intoxication
staphylococcal food posisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G., Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C., Tyree-diamensional structure of a human class II histocompatibility molecule complexed with superantigen."; Nature 368:711-718(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M11118; AAA88550.1; -
2 PIR; 827360; ENSAB6.
2 PIB; 18218.20-JUN-96.
3 PIB; 18281.20-JUN-96.
3 PIB; 18281.20-JUN-98.
4 PIB; 18281.20-JUN-97.
5 PIB; 18282.10-JUN-97.
5 PIB; 18284.11-CUCT-97.
5 PIB; 18284.11-CUCT-97.
5 PIB; 18284.11-CUCT-97.
5 PIB; 18285.28-JUN-00.
5 PIB; 18285.28-JUN-00.
5 PIB; 18285.28-JUN-00.
5 PIB; 18287.28-JUN-00.
6 PIR; 18287.28-JUN-00.
7 PIR; 18287.28-JUN-00.
7 PIR; 18287.28-JUN-00.
8 PROSITE; PSO0277; STAPH STREP_TOXIN 1; 1.
8 PROSITE; PSO0277; STAPH STREP_TOXIN 2; 1.
8 ZICHAL.
8 ZICHAL
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DQFLYEDLI -> NRFPDLIYL (IN RI
MISSING (IN REF. 3).
DIN -> NID (IN REF. 3).
OTD -> ENT (IN REF. 3).
YC -> ENT (IN REF. 3).
Y -> YY (IN REF. 3).
CE -> EQ (IN REF. 3).
D -> N (IN REF. 3).
D -> NG (IN REF. 3).
D -> ND (IN REF. 3).
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DISULEID
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                     GNHLEI PKKI VVKVSIDGIOSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY
                                                                                                                                                                                                                                                                                                                                                                                                                     QODPDESQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGP---NYD
                                                                                                                                                                                                                                                                                                                                                   30 QPDPXPDELHKSSKPTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYD
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                        Query Match
48.6%; Score 572; DB 1; Length 266;
Best Local Similarity 49.2%; Pred. No. 9e-37;
Matches 116; Conservative 36; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                          31436 MW; B6D417F61CF018B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETC3 STRAM

ID ETC3 STRAM

ID CAN STRAM

O1-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type C-3 precursor (SEC3).

GN ENTC3 OR SAV2009 OR SA1817.

OS Staphylococcus aureus (strain Mu50 / ATC7 700699),

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

ON NORL TAXID=158879, 158879, 1280;
 STRAND
HELLIX
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QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSG---PNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Struct. Biol. 2:680-686(1995).
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PDB; 1STE; 23-DEC-96.
PDB; 1SE2; 08-MAR-96.
PDB; 1CQV; 19-SEP-01.
PDB; 114P; 19-SEP-01.
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P34071;
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H
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Nature 384:188-192(1996).
-!- FUNCTION Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
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SEQUENCE FROM N.A.
STRAIN=MLSO / ATCC 700599, and N315;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Kuroda M., Ohta T., Uchiyama I., Baba T., Itan J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Samano T., Inoue R.-I., Rooyama A., Kanehisa M., Yamashita A., Oohima K., Furuya K., Yoshino C., Sekimizu K., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Fornya K., Yoshino C., Shiba Jaurels M., Ogasawara N., Hayashi H., Hiramatsu K.; Schino C., Shiba Jaurels M., Ogasawara N., Hayashi H., Hiramatsu K.; Schino C., Shiba Jaurels M., Ogasawara N., Hayashi H., Hiramatsu K.; Schino C., Shiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schino C., Shiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba Jaurels M., Osasawara N., Hayashi H., Hiramatsu K.; Schiba M., Mayashi M., Mayashi H., Hiramatsu K.; Schiba M., Mayashi M., Mayas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOCRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR. MEDLINE=97064178; PubMed=8906797; Pields B.A., Marlohiodi B.L., Li H., Ysern X., Stauffacher C.V., Schlievert P.M., Karjalainen K., Mariuzza R.A.; "Crystal structure of a T-cell receptor beta-chain complexed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hovde C.J., Hackett S.P., Bohach G.A., "Nucleotide sequence of the staphylococcal enterotoxin C3 sequence comparison of all three type C staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
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PERS 1JCK 12-NOV-97.

PERS 1KLG; 02-AUG-02.

INTERPO 1 IPRO06192; Bact_endotox.

INTERPO 1 IPRO06192; Bact_endotox.

INTERPO 1 IPRO06123; Stapl/Strept toxin.

INTERPO 1 IPRO06126; Stapl/Strept toxin.

INTERPO 1 IPRO06126; Stapl/Strept toxin.

INTERPO 1 IPRO06127; Stapl/Strept toxin.

PÉAM; PRO1123; Stapl Strp tox C; 1.

PÉAM; PRO1123; Stapl Strp tox C; 1.

PRINTS; PRO0279; BACTRIONIN.

PROSITE; PRO0279; STAPH_STREP_TOXIN 1; 1.

PROSITE; PRO0279; STAPH_STREP_TOXIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Gen. Genet. 220:329-333(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90220508; PubMed=2325627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003364; BAB58171.1; -.
EMBL; AP003135; BAB43097.1; -.
EMBL; X51661; CAA35972.1; -.
PIR; S11885; S11885.
                                                                                                                                                                                                                                                                                                                                                Lancet 357:1225-1240(2001).
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SEQUENCE FROM N.A.
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Best Local Simi
Matches 111;
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111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
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30 QPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPARISON OF STRUCTURE OF SEA AND SEC2.

MEDLINE=97334373; Publed=9191070;
Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
"A structural and functional comparison of staphylococcal
enterotoxins A and C2 reveals remarkable similarity and
dissimilarity.";
J. Mol. Biol. 269:270-280(1997).
-! FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
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-! SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                        90 KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
                                                                                                           KLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGNH
                                                                                                                                                                                                                                                                                                                                                                                                                       169 TGYIKPIPKNKESFWPDFFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 TGYIKEIENNGNTFWYDYMPAPGDKFDQSKYLMYNDNKTVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
MEDLINE-89277549; PubMed=2543637;
Bohach G.A., Schlievert P.M.;
"Conservation of the biogically active portions of staphylococcal enterctoxins of and C2.";
Infect. Immun. 57:2249-2252(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDINE=$6027099; PubMed=7582894;
Papagecorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
Brehm R.D., Tranter H.S.;
"Crystal structure of the superantigen enterotoxin C2 from
"Crystal structure of the superantigen sterotoxin C2 from
Staphylococcus aureus reveals a zinc-binding site.";
Structure 3:769-779(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96022987; PubMed=7552730;
Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Residues defining V beta specificity in staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Exterotoxin type C-2 precursor (SEC2).
ENTC2.
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150 FDNGNLQNYLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSYE 209
111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Enterotoxin type C-1 precursor (SEC1).
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InterPro; IPR008992; Bact_endotox.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006123; Stap/Strept_tox.
InterPro; IPR006123; Stap/Strept_tox.
InterPro; IPR006126; Stap/Strept_tox.
InterPro; IPR006173; Stap/Strept_tox.
IPEm; PF01123; Stap Strp_tox.
IPEm; PF0123; Stap Strp_Tox.
IPEm; PF0234; Stap 
                                                                                                                                                                                                                                                         266 AA
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                                                                                                                                                                                                                                                    ETC1 STAAU
P01553;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 QPDFTPDELHKSSEFTGTWGNWKYLYDDHYVSATKVWSVDKFLAHDLIYNISDKKLKNYD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
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R PDB; 114Q; 19-SEP-01.

R PDB; 114X; 19-SEP-01.

R PDB; 114X; 19-SEP-01.

R InterPro; 1PR008992; Bact endotox.

InterPro; 1PR006123; Stap/Strep_toxin.

InterPro; 1PR006123; Stap/Strep_toxin.

InterPro; 1PR006173; Staph tox_OB.

R InterPro; 1PR006173; Staph tox_OB.

R Pfam; PP01221; Stap Strp_tox C3.

R Pfam; PP01221; Stap Strp_tox C3.

R PRINTS; PR00279; BACTRITOXIN.

R PROSITE; PS00277; STAPH STREP_TOXIN.1; 1.

R PROSITE; PS00277; STAPH STREP_TOXIN.2; 1.

R PROSITE; PS00277; STAPH STREP_TOXIN.2; 1.

R PROSITE; PS00277; STAPH STREP_TOXIN.2; 1.
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252
256
266 AA;
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Matches 109; Conserv
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SIGNAL
CHAIN 2
DISULFID 12
METAL 3
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MEDDLINE-83213327; PubMed=6189824;
Schmidt J.J., Spero L.;
Schmidt J.J., Spero L.;
The complete amino acid sequence of staphylococcal enterotoxin Cl.";
J. Biol. Chem. 258:6300-6306(1983).
-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
169 TGYIKFIPKNKESFWFDFFPPP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                              264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88038352; PubMed=2823067;
Bohach G.A., Schlievert P.M.;
Mudleotide sequence of the staphylococcal enterotoxin Cl gene and
relatedness to other progenic toxins.";
Mol. Gen. Genet. 209:15-20(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                             TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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46.8%; Pred. No. 1.7e-34;
ive 44; Mismatches 67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCSI_TaxID=1280;
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Best Local Similarity
Matches 110; Conserv
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G89968; G89968

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                                                                          110
                                                                                                        149
                                                                                                                                    111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                 209
                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
                                     30 QPDPTPDELHKASKFTGLMENMKVLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD
                                                                                          QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSG---PNYD
                                                                           KLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGNH
                                                                                                                                                                                               TGYIKFIPKNKESFWFDFFPFF--EFTQSKYLMIYKDNETLDSNTSQIEVYLITK 221
                                                                                                                                                                                                              TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T., Matsumaru H., Maruyama A., Murakani H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kaito C., Kanenisa M., Yamashita A., Oghima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Humatsu K., Humatsu K., Humatsu K., Hankole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FRI572;
MEDLINE=98298056; PubMed=9632603;
Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
Identification and characterization of staphylococcal enterotoxin types G and I from Staphylococcus aureus.";
Infect. Immun. 66:3337-3348(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted, SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                               Enterctoxin type G precureor (SEG).
ENTG OR SEG OR SAV1824 OR SA1642.
Staphylococcus aureus (strain Mu50 / ATCC 700699)
Staphylococcus aureus (strain N315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacieria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158878, 158879, 1280;
                                                                                                                                                                                                                                                                                                                                    (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                          258 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aureus.";
Lancet 357:1225-1240(2001);
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
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28-FEB-2003
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EMBL; AF064773; AAC26660.1; -. EMBL; AP003363; BAB57986.1; -. EMBL; AP003135; BAB42910.1; -.

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57 KLKTELKNOEMATLPKDKNVDIYGVEYYHLCYLCENAE-----RSACIYGGVTNHEGNH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 -ERDKLITVQVTIDNRQSLGFTITTNKAMVTIQELDYKARHWLTKEKKLYEFDGSAFESG 204
                                                                                                                                                                                                                                                                                                                                                                                                         1 QODPDPSQLHRSSLVKN----LQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                  26 QPDPKLDELNKVSDYKNNKGTMGNVMNLYTSPPVEGRGVINSRQFLSHDLIFPIEVKSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S6 EVKTELENTELANNYKDKKVDIFGVPYFYTCIIPKSEPDINQNFGGCCMYGGLTFNSSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 LEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETG
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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EMBO J. 15:6812-6840(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=89359112; PubMed=2549000; Bayles K.W., Iandolo J.J.; "Genetic and molecular analyses of the gene encoding staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 23235;
MEDLINE=97157473; PubMed=9003758;
Sundstroem M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 YIKFIPKNKESFWFDPFPEPE---FTQSKYLMIYKDNETLDSNTSQIBVYLTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 YIKFTEKNNTSFWFDLFPKKELVPFVPXFLNIYGDNKVVDSKSIKMEVFLNT 257
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SEQUENCE PROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
nuterPro; 1PR00892; Bact_endotox.
InterPro; 1PR00812; Bact_endotox.
InterPro; 1PR006123; Stap/Strept_toxin.
InterPro; 1PR006123; Stap/Strept_toxin.
InterPro; 1PR006173; Staph tox_0B.
Pfam; PR02676; Stap_Strp_tox_C.
Pfam; PR01123; Stap_Strp_tox_C.
PR081123; Stap_Strp_tox_C.
PR08118; PR00279; BACTRLTOXIN.
PR08118; PR00279; STAPH STREP_TOXIN.
PR08118; PR00278; STAPH STREP_TOXIN.
Enterctoxin; Toxin; Signal; Superantigen; Complete proteome.
                                                                                                                                                                                                                                                                                                                         ; Score 468; DB 1; Length 258; ; Pred. No. 7.4e-29; 39; Mismatches 78; Indels
                                                                                                                                                                                                                                                                 133 BY SIMILARITY.
29940 MW; E2982101701D012C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1280,
                                                                                                                                                                                                                                                  ENTEROTOXIN TYPE G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MRA-2204 (Rel. 43, Last annotation update)
Enterotoxin type D precursor (SED).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin D.";
J. Bacteriol. 171:4799-4806(1989)
                                                                                                                                                                                                                                                                                                                                  39.7%;
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 43.89 tes 102; Conservative
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116 1
258 AA;
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Best Local S
Matches 102
                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                    CHAIN
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Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enterotoxins.";
Nat. Struct. Biol. 2:680-686(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP004828; BAB95754.1; -. EMBL; M18970; AAA26681.1; -.
                                                                                                                                                                                                                                                                                                                                          type A.";
EMBO J. 14:3292-3301(1995).
Yamamoto K., Hiramatsu K.;
                                        Lancet 359:1819-1827(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-STRUCTURE MODELING
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dissimilarity.
                          acquired MRSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 INFNSKEMAQHFKSKOVDVYPIRYSINCYGGE-IDRTACTYGGVTPHEGNKLKERKKIPI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 ELHKKSELSSTALNNMKHSY--ADKNPIIGENKSTGDQFLENTLLYKKFFTDLINFEDLL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLHR-----SSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYN---VSGPNYDKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
   SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 333.5; DB 1; Length 258;
Pred. No. 1.4e-18;
2; Mismatches 86; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 PKNKESFWFDFFPEFFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                114 P -> A (IN STRAIN ATCC 23235).
29746 MW; 4F7C6A28D42597FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P13163; ISXT.
InterPro; IPR00892; Bact_endotox.
InterPro; IPR006123; Bact_endotox.
InterPro; IPR006123; Bact_endotox.
InterPro; IPR006123; Bap/Strept_tox.
InterPro; IPR006126; Bap/Strept_tox.
InterPro; IPR006126; Bap/Strept_tox.
InterPro; IPR00127; Stap/Strp_tox.03.
Pfam; PF01123; Stap_Strp_tox.03.
Pfam; PF01123; Stap_Strp_tox.11.
PR081TE; PS00277; BACTR.TOXIN.
PR0S1TE; PS00277; STAPH_STREP_TOXIN.1; 1.
PR0S1TE; PS00277; STAPH_STREP_TOXIN.2; 1.
Enterotoxin; Toxin; Signal; Superantigen; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain MM2), and
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620, 1280;
                                                                                                                                                                                                                                                                                                                                                                                   ENTEROTOXIN TYPE D ZINC. ZINC. ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-07N-1990 (Rel. 13, Created)
01-07N-1990 (Rel. 13, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
ELECTOCXIN type A precursor (SEA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%;
                                                                                                                                                              EMBL; M28521; AAB06195.1; -.
PIR; A33953; A33953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83; Conservative
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212 2
250 2
252 2
114 1
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P13163;
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-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poleoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
-:- SUBUNIT: Monomer.
-:- SUBCELLULAR LOCATION: Secreted.
-:- SINCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
-:- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
STRAIN=FRI337;
MEDLINE=88086892; PubMed=3335483;
BetLey M.J., Mekalanos J.J.;
"Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
"Bacteriol, 170:34-41(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEARY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=97113025; PubMed=8943278;
Sunderroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
Abrahmsen L.;
"The Co-crystal structure of staphylococcal enterotoxin type A with
Zn2+ at 2.7-A resolution. Implications for major histocompatibility
Complex class II binding."
J. Biol. Chem. 271:32212-32216 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=95354648; PubMed=7628431;
Schad E.M., Zattseva I., Zattsev V.N., Dohlsten M., Kalland T.,
Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
"Crystal structure of the superantigen staphylococcal enterotoxin
                                                                                                                                                                           SEQUENCE OF 25-257.
MEDLINE=87222293; PubMed=3584106;
Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
"Complete amino acid sequence of staphylococcal enterotoxin A.";
J. Biol. Chem. 262:7006-7013(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R., "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=56022987; PubMed=7552730;
Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Residues defining V beta specificity in staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPARISON OF STRUCTURE OF SEA AND SEC2. MEDLINE-97334373; PubMed-9191070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A28664; A28664.
PDB; IESF; 11-JUL-96
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STDIVDKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWL 155

64 NQEMATLFKDKNYDIYGVEYYHLCYLCENAERSACIYGGYTNHEGNHLEIPKKIVVKVSI 123

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| Property | 1987 | 1987 | 1987 | 1987 | 1988 | 1988 | 1988 | 1989 | 1987 | 1989 | 1987 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 1989 | 198
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                                                                                                                                                                                                                                                                    GENERICULARIA GENERAL J. 170:2954-2960 (1988).

[2] Bacteriol. 170:2954-2960 (1988).

[3] STRUCTURE MODELING.

Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;

Residues defining V beta specificity in staphylococcal

enterctoxins.;

Nat. Struct. Biol. 2:680-686 (1995).

-I. FUNCTION: Staphylococcal enterctoxins cause the intoxication

staphylococcal food poisoning syndrome. The illness characterized

by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II (By similarity).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-88257005; PubMed=3384800;
Couch J.L., Soltis M.T., Betley M.J.;
"Cloning and nucleotide sequence of the type E staphylococcal
                                                                                                             Staphylococcus auxeus.
Bacteria: Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
                                                      01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Enterotoxin type E precursor (SEE).
                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
STRAIN=MJB265;
                            STANDARD;
                                                                                                                                                                                                                                                              enterotoxin gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.
                            STAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                    death
               ETXE_STAAU
RESULT
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8 6

Query Match

24.9%; Score 293.5; DB 1; Length 257;
Best Local Similarity 33.0%; Pred. No. 1.5e-15;
Matches 73; Conservative 43; Mismatches 94; Indels 11.

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X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).

MEDLINE=2044256; PubMed=10986116;

MEDLINE=2044256; PubMed=10986116;

Antonsson M., Petersson K.,

Antonsson P., Svensson L.A.;

Antonsson P., Svensson L.A.;

"The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TcR molecules.";

J. Mol. Biol. 302:527-537(2000).

-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
-1- SUBCELLULAR LOCATION: Secrete Server Server 1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                              STRAIN=D4508;
MEDILNE=28053699; PubMed=7964453;
MEDILNE=28053699; PubMed=7964453;
Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
Fischetti V.A., Zabriskie J.B.;
"Characterization and biological properties of a new staphylococcal
                                                                                                                                                                                                                                                                                                             STRAIN=NWD;

BUDINE-22040717; PubMed=12044378;

Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,

Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,

Samamoto K., Hiramatsu K.;

"Genome and virulence determinants of high virulence community-
acquired MRSA.";
                                                                                                                               SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
Enterotoxin type H precursor (SEH).
ENTH OR SEH OR MW0051.
Staphylococcus aureus (strain MW2), and
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620, 1280;
                                                                                                                                                                                                                                                      Exp. Med. 180;1675-1683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 359:1819-1827(2002).
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               death
                                                                                                                                                                                                                                          exotoxin.
     244
247
257
29358 MW; 27EDA94E97770CE3 CRC64;
                                     ENTEROTOXIN TYPE E.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                     \begin{array}{c} 0.223 \\ 0.223 \\ 0.231428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.24428 \\ 0.
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245
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257 AA;
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METAL
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| R EMBL, AP004822; BAB93916.1; -...
| PBB; IENF; 10-JAN.01. |
| PBB; IENF; 10-JAN.01. |
| R PROFICE; 1PRO06127; Bact endotox. |
| InterPro; 1PRO06127; Bact Exp. toxin. |
| InterPro; 1PRO06127; Stap. Cox.05. |
| R PRO1827; Stap. Strp. toxin. |
| R PRO1827; Stap. Strp. toxin. |
| R PRO1827; Stap. Strp. toxin. |
| R PRO1827; STAPH STREP TOXIN. |
| R PROSTTE; PS00279; BACTRITOXIN. |
| R PROSTTE; PS00279; STAPH STREP TOXIN. |
| R PROSTTE; PS00279; STAPH 124 DGIQ-SLSFD-IETNKKMVTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179 64 NOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 123 7 SOLHRSSLVKNLONIYFLYEGDPVTHENVKSVDQLLSHHLIYN---VSGPNYDKLKTELK 63 Query Match 24.7%; Score 291.5; DB 1; Length 257; Best Local Similarity 35.1%; Pred. No. 2.2e-15; Matches 79; Conservative 42; Mismatches 85; Indels 19; 180 ESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220 (Rel. 43, Created) (Rel. 43, Last sequence update) (Rel. 43, Last annotation update) PRT; 241 AA STANDARD;

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RESULT 10 ETXH STAAN ID ETXH STAAN AC QS338E; DT 15-MAR-2004 (DT 15-MAR-2004 (

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InterPro; IPR008992; Bact_endotox.
InterPro; IPR006128; Staph/Strept_toxin.
InterPro; IPR006128; Staph/Strept_toxin.
InterPro; IPR006128; Staph, Strept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Stap_Strp_tox_O; I.
PR0SITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
PR0SITE; PS00278; STAPH_STREP_TOXIN_2; I.
PQTENTIAL.
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STRAIN=SF370 / ArCC 700294 / Serctype M1;
STRAIN=SF370 / ArCC 700294 / Serctype M1;
STRAIN=SF370 / ArCC 700294 / Serctype M1;
SECRETE 119264; PubMed=11296296;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Secate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olia H.G., Najar F.Z., Red Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 9814658+463 (2001).
--- SUBUNIT: Binds to major histocompatibility complex class II beta
                                                                                                                                         27 IHDKSELTDLALANAYGQY-NHPPIKENIKSDEISGEKDLIFRNQGDSGNDLRVKFATAD
                                                                                                                                                                                                                                                                        9 LHRSSLVKN--LQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKTELKNQE
                                                                                                                                                                                                    125 GIOSLSFDIETNKKANTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99093428; PubMed=9874566;
Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
"Identification and characterization of novel superantigens from
                                                                         17;
                                         DB 1; Length 241;
                                   Match 23.9%; Score 281.5; DB 1; Length Local Similarity 38.0%; Pred. No. 1.2e-14; les 84; Conservative 33; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria, Pirmicutes, Lactobacillales; Streptococcaceae;
   27858 MW; 70F77985877616CE CRC64;
                                                                                                                                                                                                                                                                                                                           185 DFFP---EPEFTQSKYLMIYKDNETLDS-NTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
SPEH OR SPY1008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes.";
J. Exp. Med. 189:89-102(1999).
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     241 AA;
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Q9X5C8;
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EMBL, AF124500; AAD30989.1; -. EMBL, AE006546; AAX33907.1; -. PDB; 1ET9; 24-MAY.00. PDB; 1EU4; 24-MAY.00.

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131
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                                                                                                                                                                                                                                                                                                           149 FITVNKPKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKGTVTLDLNSGKDIVFDLYYFGN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIRAIN-SERIO, M.A..
SIRAIN-SERIO, M.A..
MEDLINE-21192684, PubMed=11296296,
MEDLINE-21192684, PubMed=11296296,
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar E.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
"Complete genome sequence of an M1 strain of Streptococcus
                                                                                                                                                                                                         74 KNVDIYGVEYYHLCYLCENAERSACIYGGV--TNHEGNHLEIPKKIVVKVSIDGIQSLSF
                                                                                                                                                                                                                                              96 KEVDIYALSAQEVCE-CPGKRYEA--FGGITLINSEKKEIKVP----VNVWDKSKQQPPM
                                                                                                                                17 NLONIYFLYEGDP--VTHENVK-SVDQLLSHHLIYNVSGPNYDKLKTELKNQEMATLFKD
                                                                                                                                                                   39 NRHNLESLYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKN---LSVFFEKDWISQEFKD
                                                                                           Gaps
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MEDILINE=22363541, PubMed=1500157;

Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Molecular population genetic evidence of horizontal spread of two

alleles of the pyrogenic exotoxin C gene (spec) among pathogenic

clones of Streptococcus pyogens";

Infect. Immun. 60:3513-3517(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88314303; PubMed=3045005; Gobborn S.C., Schlievert P.M.; "Nucleotide sequence of streptococcal pyrogenic exotoxin type C."; Infect. Immun. 56:2518-2520(1988).
                                                                                           19;
                                                         Length 236;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                236 AA; 27485 MW; 16352923907AD40D CRC64;
                                                         DB 1;
                                                    17.8%; Score 209.5; DB 1;
31.4%; Pred. No. 3.5e-09;
rative 32; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN'-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Exctoxin type C precursor (SPE C).
EXOTOXIN TYPE H.
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                                                                     Similarity 31.4°
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NCBI_TaxID=1314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRPY
                  SEQUENCE
                                                         Query Match
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Matches 6
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ACRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.

MEDLINE=9739735; PubMed=9253413;
ROUSSEL A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
ROUSSEL A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
"Crystal structure of the streptococcal superantigen SFB-C:
"Grystal structure of the streptococcal superantigen SFB-C:
"Grystal structure of the streptococcal interaction
with MHC class II molecules.";
Nat. Struct. Biol. 4:635-643(1997).
-; FUNCTION: Causarive agent of the symptoms associated with scarlet
fever, have been associated with streptococcal toxic shock-like
disease and may play a role in the early events of rheumatic Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001)

WOUT WEAL TO TO:OT:OU TOOK

SUBUNIT: Binds to major histocompatibility complex class II beta

-1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE. -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin

family.

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EMBL; M35514; AAA27017.1; ALT SEC. EMBL; M97156; AAB59091.1; --EMBL; M97157; AAB59092.1; --EMBL; AE006523; AAK3664.1; --PIR; A0509; A30509. PIR; A44799; A44799; PDB; LANK; 29-ARR-98. PDB; LANK; 07-JUN-02.

PUBB; MAN 1991.
PUBB; MAN 1991.
PUBB; MAN 1991.
PUBB; MAN 1992.
INTERPROFILED:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial 116 KIVVKVSIDG--IQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYINGPSKYETGYIK 173 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192664; PubMed=11296296;
Ferretti J.G., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Oian H.G., Najar F.Z., McLaughlin R., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 9814568+4663(2001).
-!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.
-!- SUBUNIT: Binds to major histocompatibility complex class II beta 22 SPIIKSDSKKDISNVKSDLLYAYTITPYDYKNCR-VNFSTTHTL--NIDTQKYRGKDYYI KTELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVT---NHEGNHLEIPK SQLHRSSLVKNLQNI----YFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYD----KL Gaps chain. -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family. STRAIN=M1;
MEDLINE=99093428; PubMed=9874566;
Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
"Identification and characterization of novel superantigens from 30; 174 FIPKNKESFWFDFFPEP-EFTQSKYLMIYKDNETLD-SNTSQIEVYL 218 17.4%; Score 205; DB 1; Length 235; 29.5%; Pred. No. 7.7e-09; ive 47; Mismatches 83; Indels Streptococcus pyogenes. Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, 27371 MW; 070534ABB952C1E0 CRC64; 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-OCT-2001 (Rel. 40, Last annotation update)
SPEG OR SPY0212. Streptococcus pyogenes."; J. Exp. Med. 189:89-102(1999). Query Match
Query Match
Best Local Similarity 29,50,
Best Local Similarity 29,50, 190 194 194 204 213 220 220 223 226 226 235 AA; SEQUENCE FROM N.A. Streptococcus. NCBI_TaxID=1314; RESULT 13 SPEG STRPY ID SPEG STRPY AC Q9X5C7; TURN STRAND TURN HELIX STRAND HELIX STRAND STRAND SEQUENCE 59 SOLUTION g 8 d 8 6 ठ g

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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 -TLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNH--EGNHLEIPKKIVVKVSIDG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 IQSL--SFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 KETYLPSEAVRIKKKOFTLOEFDFKIRKFLMEKYNIÝ-DSESRÝTSGSLFLATKDSKHYE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 ENVKSVDQLLSHHLIYNVSGPNYDK-----LKTELKNQEMA-----
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MEDLINE=87057222; PubMed=3782090;
Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
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MDELLINE-84150589; PubMed=8107781;
Acharya K.R., Passalactus E.F., Jones B.Y., Harlos K., Stuart D.I., Brehm R.D., Tranter H.S.;
Structural basis of superantigen action inferred from crystal structure of toxic-shock syndrome toxin-1.";
Nature 367:94-97(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.8%; Score 162; DB 1; Length 234; Best Local Similarity 24.1%; Pred. No. 1.5e-05; Matches 53; Conservative 42; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN 25 234 EXOTOXIN TYPE G. SEQUENCE 234 AA; 27262 MM; 49525C49E4BA2052 CRC64;
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NCBI_TaxID=1280;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-WAR-2004 (Rel. 43) Last annotation update)
Toxic shock syndrome toxin-1 precursor (TSST-1).
entities requires a license agreement (St
or send an email to license@isb-sib.ch).
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MEDLINE=94092653; PubMed=8268150;
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PO6886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **ARY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
MEDLINE=9825504; PubMed=9585531;
Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
Schlievert P.M., Ohlendorf D.H.;
"Structures of five mutants of toxic shock syndrome toxin-1 with
reduced biological activity.",
"Structures of five mutants of toxic shock syndrome toxin-1 with
seduced biological activity.",
-i- SUGCELIULAR LOCATION: Secreted.
-i- SUBCELIULAR LOCATION: Secreted.
-i- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.
Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlivert P.M., Oblandorf D.H., B.H., "Structure of toxic shock syndrome toxin 1.", Biochemietry 32:13761-13766(1993).
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MEDLINE=9737442; PubMed=9194182;
Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
Dinges M.M., Cook W.J., Schlivert P.M., Ohlendorf D.H.;
Takfinds structures of three crystal forms of toxic shock syndrome toxin-1 and of a tetramutant with reduced activity.";
Protein Sci. 6:1220-1237(1997).
                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
MEDIINE=96319751; PubMed=8759320;
MEDIINE=96319751; PubMed=8759320;
Acharya K.R.;
The refined crystal structure of toxic shock syndrome toxin-1 at 2.07-A resolution.";
J. Mol. Biol. 260:553-569(1996).
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PDB; 3TSS; 24-DEC-97.
PDB; 4TSS; 24-DEC-97.
PDB; 4TSS; 24-DEC-97.
PDB; 5TSS; 24-DEC-97.
PDB; 5TSS; 24-DEC-97.
PDB; 1011; 12-AUG-97.
PDB; 1011; 12-AUG-97.
PDB; 1TSS; 16-DEC-98.
PROFIGE PROFIGES; Staph_toxin.
PEAM; PF01123; Staph_toxin.
PEAM; PF01123; Staph_toxin.
PROFITE; PS00127; TXTAPH_STREP_TOXIN_1; PRINTS; PROFICES.
POWATH; PROFICES.
PDB; 1TSP; PS001279; TXTAPH_STREP_TOXIN_2; 1.
PROFITE; PS001279; TAPPH_STREP_TOXIN_2; 1.
PAGFITE; PS001279; TAPPH_PS0127050; 1.
PAGFITE; PS001279; TAP
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SIGNAL
CHAIN 41 234 TOXIC SHOCK SY
HELIX 46 59
TIRAND 58 69
STRAND 72 71
STRAND 72 71
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SÍGNAL
PROPEP
CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
53 -----pNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 SLIIFPSPYYSPAFTKGEKVDLNTKRTKKSQHTSEGTYIHF------QISGVTN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 HEGNHLEIPKKIVVKVSIDGIQS-LSFDIETNKKOMTAQELDYKVRKYLTDNKQLYTNGP 164
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22.6%; Pred. No. 0.65;
tive 31; Mismatches 99; Indels 34; Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Desmocollin 1A/1B precursor (Desmosowal glycoprotein 2/3) (DG2/DG3)
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Theis D.G., Koch P.J., Franke W.W.;
"Differential synthesis of type 1 and type 2 desmocollin mRNAs in human stratified epithelia.";
Int. J. Dev. Biol. 37:101-110(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                        26306 MW; E95789FF9A1D7AB4 CRC64;
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Best Local Similarity 22...
Best A8; Conservative
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TISSUE=Foreskin;
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      DSC1_HUMAN
Q08554;
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SEQUENCE
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A Simbelhamm R. Simbelhamm R.
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Query Match

8.6%; Score 101; DB 1; Length 894;
Best Local Similarity 19.8%; Pred. No. 3.2;
Matches 51; Conservative 43; Mismatches 79; Indels 84; Gaps 10;
                                                                                                                                                                                                                                                                                                186 YIEKOTGDIFCTRSIDREKYEQF------ALYGYATTADGYAPEYPLFLIKI 232
                                                                                                                                                                                                                                                                                                                                       122 SIDGIQSLSFDIE-----TUNKANVTAQELD------YKVRKYLTDNKQ 158
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                                                                                                                                                                                                                                                                                                                                                                                                                      293 HFSIHP---DIGVITTIPFLDREKCDIYQLIMEVRDMGGQPFGLFNTGTITISLEDEND 349
                                                                                                                                                                                                                                      64 NOEWAT -- LEKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKV 121
                                                                                                                                                                                                                    4 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLLYNVSGPNYDKLKTELK 63
CADHERIN 5.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
KVYLCGQDEEH -> ESIRGHTLIKN (in isoform
                                                       1B). | FIId=VSP 000651. | Missing (In isoform 1B). | FTId=VSP 000652. | 132 | T - S (IN REF. 3). | 894 AA; 100044 MW; 44BA33038699BEEI CRC64;
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350 NPPSFTETSYVTEVEEN 366
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Search completed: May 7, 2004, 12:08:08 Job time : 19 secs

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SECUENCE FROM N.A.
STRAIR-SSI-1, A Serotype M3;
Nakata M., Tomiyèeu Y., Yapeshita A.,
Nakagawa I., Kurokawa K., Nakata M., Tomiyèeu Y., Yapeshita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunbaga T. Hattori M.,
Hayashi H., Hamada S.,
The genome of invasive Streptococcus pyogenes; a comparative analysis of S. pyogenes SSI-1, SF370 and MGAS9232.",
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE014161; AAM79908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22133808; PubMed=12122206;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barzblan K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a sercitype M3 strain of froup A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                    01-007-2002 (TrEMBLrel. 22, Created)
01-007-2003 (TrEMBLrel. 22, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Exotoxin type A-phage associated (SpeA precursor).
SPEA3 OR SPYM3 1301 OR SPS0560.
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Proc. Natl, Acad. Sci. U.S.A. 99:10078-100/83(2002).
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Q9R5X4
Q504534
Q504739
Q54739
Q54739
Q98ZZA
Q98ZZA
Q98ZZA
Q99ZZA
Q99ZA
Q98ZA
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Q8NVM3
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                                       PRELIMINARY;
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NCBI_TaxID=198466;
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   QBK6K5;
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Q8K6K5
    Q8nxj6 staphylococ
005157 staphylococ
Q06531 staphylococ
Q06535 staphylococ
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05479 streptococc
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09731 streptococc
09524 streptococc
093854 streptococc
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09386 streptococc
09616 streptylococ
006532 staphylococ
006533 staphylococ
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                                                                   7, 2004, 12:04:53 ; Search time 46 Seconds (without alignments) 1515.859 Million cell updates/sec
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1 QODPDPSQLHRSSLVKNLQN......KDNETLDSNTSQIEVYLTTK 221
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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PIR; A60108; A60108. GO; GO:0005576; C:extracellular; IEA. GO; GO:0015070; F:toxin activity; IEA.

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61 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
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C STRAIN=MGASG4 AND MGAS158 AND MGAS491, and MGAS495;

C STRAIN=MGASG4 AND MGAS158 AND MGAS491, and MGAS495;

MEDLINE=92044323; PubMed=1940804;

A Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

Mcharacterization and clonal distribution of four alleles of the spreame encoding pyrogenic exotoxin A (scarlet fever toxin) in

Streptococcus pyrogenic exotoxin A (scarlet fever toxin) in

Streptococcus pyrogenic exotoxin A (scarlet fever toxin) in

B EMBL; X61569; CAA437671; -..

R EMBL; X61579; CAA437761; -..

R EMBL; X61571; CAA437761; -..

R EMBL; X61571; CAA437691; -..

R EMBL; X61571; CAA437691; -..

R EMBL; X61571; CAA437691; -..

R PIR; A60108; A60108.
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96.3%; Score 1134; DB 2; Length 236;
Best Local Similarity 99.5%; Pred. No. 1.5e-75;
Matches 213; Conservative 0; Mismatches 1; Indels (
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                  236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214
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                                                                                                                                                                                                                    POTENTIAL.
TYPE A EXOTOXIN.
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InterPro; IPR006173; Staph_tox_OB.
Pfam; PP01123; Stap_Strp_toxin; 1.
Pfam; PP02876; Stap_Strp_tox_C; 1.
PR01175; PR00279; BAČTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN.
PROSITE; PS002778; STAPH_STREP_TOXIN.
PROSITE; PS002778; STAPH_STREP_TOXIN.
PROSITE; PS002778; STAPH_STREP_TOXIN.
2; 1.
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GO, GO:001576; C:extracellular; IEA.
GO; GO:001576; C:extracellular; IEA.
GO; GO:001576; P:toxin activity; IEA.
GO; GO:001576; P:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IRR00892; Bact endotox.
InterPro; IRR006123; Stap/Strept.tox.
InterPro; IRR006123; Stap/Strept.tox.
Pfam; PF01123; Stap Strp toxin; I.
Pfam; PF01123; Stap Strp toxin; I.
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NCBI_TaxID=1314;
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SEQUENCE
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Q54779
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RX MEDLINE=92044323; PubMed=1940804;

RA Nelson K., Schlidever P.M., Schlander R.K., Musser J.M.;

RA Nelson K., Schlidever P.M., Schlander R.K., Musser J.M.;

RT Gene encoding pyrogenic exotoxin A (scarlet fever toxin) in

RT Streptococcus pyogenes.";

RI Streptococcus pyogenes.";

RI Streptococcus pyogenes.";

BL J. Exp. Med. 174:1271-1274(1991).

BC EMBL; X61556; CAA43754.1; ---

DR EMBL; X61559; CAA43758.1; ---

DR EMBL; X61559; CAA43758.1; ---

DR EMBL; X61559; CAA43756.1; ---

DR EMBL; X61559; CAA43756.1; ---

DR EMBL; X61559; CAA43757.1; ---

DR EMBL; X61559; CAA43757.1; ---

DR EMBL; X61559; CAA43757.1; ---

DR HSRP, PO80095; 1B1Z.

AGO: AGO-ADDRERS AGOLOS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P97163 PRELIMINARY; PRT; 236 AA.
P97165; P97164;
01-MAY-1997 (TYENBLE). 03, Last sequence update)
01-MAY-1997 (TYENBLE). 03, Last sequence update)
01-OCT-2003 (TYENBLE). 25, Last annotation update)
Type A exotoxin precursor (Fragment).
                         InterPro; IPR000992; Bact endotox.
InterPro; IPR006177; BctrI tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006124; Staph/Strep tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PP01123; Stap Strp toxin; 1.
PR0011E; PR00279; BACTRITOXIN.
PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
PROSITE; PS00278; STAPH STREP TOXIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO: GO:0005576; C:extracellular; IEA.
GO: GO:0015070; F:toxin activity; IEA.
GO: GO:001405; P:pathogenesis; IEA.
InterPro; IPR00899; Bacra endotox.
InterPro; IPR006177; Batra tox.
InterPro; IPR006137; Staph/Strept_toxin.
InterPro; IPR006123; Staph/Strept_toxin.
     P:pathogenesis; IEA
                                                                                                                                                                                                                                                                                                          Complete proteome
SEQUENCE 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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83 BLKNOEMATLFYDKNVDIYSVEYYHLCYLCENAERSACIYGGVTWHEGNHLEIFKKIVVK 142
                                                                                                                                                                                                                                                                                                                                    VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                     61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                 23 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                          1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-391799; PubMed=9952369; MEDINE-3913799; PubMed=9952369; MEDINE-39137799; PubMed=9952369; MEDINE-39137799; PubMed=9952369; MeDINE-39137799; Piorentino T.R., Caringal R.M., Hollingshead S.K., Beall B.; Forentino T.R., Actophocococi."; J. Infect. Dis. 179:627-636(1999). EMBL, ACCS699; AAD11624.1; -... FMRSP; PO8095; IBIZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 222;
                                                                                                                                           Length 236;
                                                                                                                                         95.8%; Score 1128; DB 2; Length 2
99.1%; Pred. No. 4e-75;
cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25759 MW; 48BB7ADDCD91FBA3 CRC64;
                                                                                                              236 AA; 27484 MW; 2EF7F41AAC853600 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       SFWFDFFPEPETQSKYLMIYKDNETLDSNTSQI 236
                                                                                                                                                                                                                                                                                                                                                                                                     181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOSPITE PROUDS 1 121.0

GO; GO: 0015576; C: exerracellular; IEA.
GO; GO: 0015070; F: toxin activity; IEA.
GO; GO: 000456; P: pathogenesis; IEA.
InterPro: IPR006177; Bact endotox.
InterPro: IPR006127; Bact endotox.
InterPro: IPR006128; Stap/Strept toxin.
InterPro: IPR006128; Stap/Strept toxin.
InterPro: IPR006128; Stap/Strept toxin.
InterPro: IPR006128; Stap/Strept toxin.
InterPro: IPR006139; Stap tox OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
PRMNTS; PR00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
NON TER.

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NON TER.
222 222
SEQUENCE 222 AA; 25759 WW; 48BB7ADDCD911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.5%; Score 1125;
 PS00277; STAPH_STREP_TOXIN_1; 1. PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.1
Matches 212; Conservative
PROSITE; 1
Signal.
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SIGNAL
                                                                                             NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                         83 ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 142
                                                                                                                                                                                                                                                      23 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 82
                                                                                                                                                                                                                            QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                          Score 1133; DB 2; Length 236;
Pred. No. 1.7e-75;
1; Mismatches 1; Indels (
                                                                1 1 22 POTENTIAL.
23 >236 TYPE A EXOTOXIN.
236 236 236 WW; 29DPZAD575623A84 CRC64;
 PR00279; BACTRLTOXIN.
PS00277; STAPH_STREP_TOXIN_1; 1.
PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                              96.2%;
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Matches 212; Conservative
   PRINTS; PROSITE; PROSITE; PROSITE; Signal. NON TER SIGNAL CHAIN NON TER SEQUENCE
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61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
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                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDLINE=99137798; PubMed=9952369;

NEDLINE=99137798; PubMed=9952369;

NA Hollingsdead S.K., Beall B.;

"Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci.";

"Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci.";

"Infect. Dis. 179:627-636(1999).

EMBL; AF029051; AAD21315.1; -.

REBL; AF029051; AAD21315.1; -.

REBL; AF029051; AAD21315.1; -.

REBL; AF029051; BAZ

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005965; P:pathogenesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

RO; GO:0009405; P:pathogenesis; LEA.

RO; GO:0009405; P:pathogenesis; LEA.

RO; GO:000517; BCTL LOX.

RICEPPO; IPR006127; Staph/Strept LOX.

RICEPPO; IPR006127; Staph/Strept LOX.

RICEPPO; IPR006129; Staph/Strept LOX.

REPROSTO: Staph-LOX.

REPROSTO: Staph-LOX.

REPROSTO: Staph-LOX.

REPROSTO: STAPH-STREP_TOXIN.

REPOSTO: STAPH-STREP_TOXIN.

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REPOSTO: STAPH-STREP_TOXIN.

REPROSTOR STAPH-STREP_TOXIN.
ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
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                               VSIDGIOSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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85.8%; Score 1011; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 1.4e-66;
Matches 189; Conservative 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NGBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA; 25884 MW; 121F8460992818F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Exotoxin type A (Fragment).
                                                                                                                                                                                                                                     181 SFWFDFFPEPEPTQSKYLMIYKDNETLDSNTS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
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STRAIN=D633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    098524;
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                                                                                                                                                                                                                                                        11 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIFKKIVVK 130
                                                                                                                                                                                                                                                                                                                                     121 VSIDGIQSLSFDIETNYGOVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                               SERVINE ACASISE;

X MEDINE-9204423; bubmed-1940804;

X MEDINE-9204423; bubmed-1940804;

X Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

A Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

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GO; GO:0005576; Cextracellular; IEA.

GO; GO:000577; Ectri Lox.

InterPro; IPR006123; Stap/Strept cox.

InterPro; IPR006124; Stap/Strept cox.

INTERPRO; IPR006125; BACTRLTOXIN.

INTERPRO; PR00279; BACTRLTOXIN.

INTERPROSITE; PS00277; STAPH-STREP TOXIN.

INTERPROSITE TOXIN.
                                                                                            1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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      Best Local Similarity 99.5%; Pred. No. 6.2e-75;
Matches 211; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 236
236 AA; 27575 MW; 70F54120E79127DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
TYPE A EXOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEWFDFFPEPEFTOSKYLMIYKONETLDSNTS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type A exotoxin precursor (Fragment) SPEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
>236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus.
NCBI_TaxID=1314;
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Local 5.
192;
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Matches
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Q54696
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RESULT 8

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57 KLKTELKNOEMATLFKOKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGNH 110
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MEDLINE-20566668; PubMed=11114901;
Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 LEIPK--KIVVKVSIDGIQSLSFDIETNKOMTRQELDYKVRKYLTDNKQLYTNGPSKYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 FDNGKLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QODEDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSG---PNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPURINE STORM 13.7; PubMed=8406814; MEDINE=94011313; PubMed=8406814; MART JC., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.; MART JC., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.; Tolological and evolutionary implications."; Infect. Immun. 61:4254-4262 (1993).

Infect. Immun. 61:4254-4262 (1993).

R MEMBLY L13376; AAA26620.1; -.

R HSSP, P34071; ISE2.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:000576; P:toxin activity; IEA.

GO; GO:0009405; P:toxin activity; IEA.

R InterPro; IRR06892; Bact endotox.

R InterPro; IRR066129; Staph.tox.03.

R InterPro; IRR066129; Staph.tox.03.

R Pfam; PF01287; Stap Strp.toxin; 1.

R PRINTS; RR00279; BACTRITOXIN; 1.

R PROSITE; PS00277; STAPH.STREP_TOXIN_1; 1.

R PROSITE; PS00277; STAPH.STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meaney W.J., Smyth C.J.;
"Characterization of a putative pathogenicity island from bovine "Characterization of a putative pathogenicity island from bovine graphylococcus aureus encoding multiple superantigens.";
J. Bacteriol. 183:63-76(2001).

EMBL, AF217235; AAG29599.1; -.
HSSP, PA4071; 1S22.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; P:toxin activity; IEA.
GO; GO:0005405; P:pathogeneais; IEA.
InterPro; IPR006177; Botrl tox.
InterPro; IPR006173; Stap/Strep_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 549; DB 2;
; Pred. No. 1.1e-32;
44; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcal enterotoxin C-bovine SEC-BOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.2%
Matches 111; Conservative
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FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
SEQUENCE
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Q9F0L6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                          ESCUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A Kalia A., Bessen D.E.;

Tresence of streptococcal pyrogenic exotoxin A and C genes in human isolates of group G Streptococcal.";

Submitted (AUG-2001) to the EMBL/Genbank/DDBJ databases.

Example, ANG-9745, AAL06068.1;

SEQUENCE OF CO.0005576; C:extracellular; IEA.

SEQUENCE OF CO.000405; P:pathogenesis; IEA.

SEQUENCE OF CO.000405; Staph/Strept toxin.

BR GO; GO:000405; Staph/Strept toxin.

SEQUENCE OF CO.000405; Staph/Strept tox.

DR PEAN; PRO0123; Staph toxin; 1.

DR PROSITE; PS00279; STAPH STREP TOXIN.1; 1.

DR PROSITE; PS00279; STAPH STREP TOXIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 QQDPNPSQLHRSSLVKNLQNIYFLYEGDPVVHENVKSVDQLLSHDLIXNVSGLNYDKLKT 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.8%; Score 1011; DB 2; Length 222;
89.2%; Pred. No. 1.4e-66;
iive 12; Mismatches 11; Indels
                                                                                                                                                                                                                          Streptococcus equisimilis.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 222
222 AA; 25884 MW; 121F8460992818F8 CRC64;
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Last annotation update)
                                                                                                        093894;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pyrogenic exotoxin A (Fragment).
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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                                                                                       222 AA.
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                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=119602;
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NCBI_TaxID=1280;
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Best Local Similarity 46.8%;
Matches 110; Conservative
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01-OCT-2003 (TrEMBLrel
Enterotoxin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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01-NOV-1996
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A MEDILINE=9401313; PubMed=8406814;

A Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;

T. "Characterization of novel type C staphylococcal enterotoxins:
Diological and evolutionary implications.";

Infect. Immun. 61:4254-4262(1993).

R MSLP, pa4071, 18E2.

R HSSP, pa4071, 18E2.

R GO; GO:005576; C:extracellular; IEA.

GO; GO:005576; C:extracellular; IEA.

GO; GO:005576; C:extracellular; IEA.

GO; GO:005576; C:extracellular.

R GO; GO:0015070; P:toxin activity; IEA.

GO; GO:0015070; P:toxin activity; IEA.

InterPro; IPR006173; Btrd Lox.

INTERPRO; IPR006173; Strd Lox.

INTERPRO; IPR006173; Strd Lox.

INTERPRO; IPR006173; Strd Lox.

INTERPRO; IPR006173; Strd Lox.

INTERPRO; IPR00775; STRPH_STREP_TOXIN.

PRINTS; PR00277; STRPH_STREP_TOXIN.

PROSITE; PS00277; STAPH_STREP_TOXIN.

INTERPRO; IPR00778; STAPH_STREP_TOXIN.

PROSITE; PS00277; STAPH_STREP_TOXIN.
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                                                                                                                                                                                                                                                                     Ouery Match
46.6%; Score 549; DB 2; Length 271;
Best Local Similarity 47.2%; Pred. No. 1.3e-32;
Matches 111; Conservative 44; Mismatches 66; Indels 14;
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         InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph.tox.OB.
Pfam; PF012123; Stap_Strp_tox.O; 1.
Pfam; PR02176; Stap_Strp_tox.C; 1.
PRINTS; PR00279; BACTRL/TOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
SEQUENCE 271 AA; 31267 MW; 3493F622BB042F10 CRC64;
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(TremBirel. 01, Last sequence update)
(TremBirel. 25, Last annotation update)
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Best Local Similarity 47.2%
Matches 111; Conservative
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01-OCT-2003
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SEQUENCE
                                                                                                                                                                                                                                                                                 Query Match
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006532
AC 006532,
DT 01-NOV-
DT 01-OCT-
DE EAGEPOUL
OC Bacterio
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QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSG-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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                                                                                                                168
                                                                                                                                                  123 FDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                     122
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                               111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKKNTAQELDYKVRKYLTDNKQLYTNGPSKYF
57 KLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLC.-ENAER----SACIYGGVTNHEGNH
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                                                                                                                                                                                                                                    TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLITK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P SEQUENCE FROM N.A.,

WEDLINE=94011313; PubMed=8406814;

WEDLINE=94011313; PubMed=8406814;

MEDLINE=94011313; PubMed=8406814;

MEDLINE=94011313; PubMed=8406814;

MEDLINE=94011313; PubMed=8406814;

The Characterization of novel type C staphylococcal enterotoxins:

It infect. Immun. 61:4254-462(1993).

REMEL; 1.13378; AAA26622.1; -

REMEL; 1.13378; AAA26622.1; -

REMEL; 1.13378; AAA26622.1; -

REMEL; 1.13378; PAA26622.1; -

REMEL; 1.13378; PAA26622.1; -

REMEL; 1.13378; PAA26622.1; -

REMEL; 1.13378; PROMOS576; C:extracellular; IEA.

REMEL; 1.18006576; C:extracellular; IEA.

REMEL; 1.18006177; REMEL; Lox.

REMEPRO; IPRO06123; Stap/Strep_toxin.

REMEPRO; IPRO06124; Stap/Strep_toxin.

REMEPRO; IPRO06124; Stap/Strep_toxin.

REMEPRO; IPRO06173; Stap/Strep_toxin.

REMEPRO; REMEPROST6; Extep_toxin.

REMITYS; PRO02779; BACTHLOXIN.

REMITYS; PRO02779; RAPH_STREP_TOXIN.2; 1.

ROSSITE; PSO0277; STAPH_STREP_TOXIN.2; 1.
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46.8%; Pred. No. 1.6e-32;
.ive 44; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA; 27651 MW; A21A954386AE8625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Matches 112; Conservative
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Best Local Símilaríty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 FDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKALYEFNSSPYE 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 QPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVKSKVDKFLAHDLIYNISDKKLKNYD 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 TGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMMYNDNKTVDSKRVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tagnamoro K., Hiramateu K.; Manni I.; Manni I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; FubMed=12044378;
MEDLINE=22040717; FubMed=12044378;
MEDLINE=22040717; FubMed=12044378;
Magal Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
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                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUJ-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type C enterotoxin (Fragment)
Staphylococcus intermedius
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=196620;
                                                                                                             266 AA.
                                                                                                                                                                                                                                                                                                                                                                          Enterotoxin type C precursor.
SEC4 OR MW0759.
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                                                                                                             PRELIMINARY;
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RESULT 13
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123 FDNGNLQNVLIRVYENKRNTISFDVQTDKKSVTAQELDIKARNFLINKKNLYBFNSSPYE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
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Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
"Characterization of the type C enterotoxin (SEC-canine) produced by Staphylococcus intermedius pyoderma isolates.";
Submitted (FEB-1897) to the EMBL/GenBank/DDBJ databases.
EMBL: U91526; ABS50248:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGENOME STRAINS AND STRAINS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.3%; Score 546; DB 2; Length 239; 47.7%; Pred. No. 1.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        006531;
0.NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                              GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0015070; F: toxin activity; IEA.
GO; GO: 0015070; F: pathogenesis IEA.
InterPro; IPR00619; Bact endotox.
InterPro; IPR00619; Bact toxin.
InterPro; IPR006123; Baph/Strept toxin.
InterPro; IPR006123; Staph/Strept toxin.
InterPro; IPR006125; Staph/Strept toxin.
InterPro; IPR006123; Staph/Strept toxin.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF01123; Stap Strp toxin; 1.
PR0311E; PR00279; BACTRITOXIN.
PROSITE; PS00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.
PR0511E; PS00278; STAPH_STREP_TOXIN_2; 1.
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us-10-625-221-14.rspt

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Mon May 10 16:02:39 2004
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111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRXYLTDNKQLYTNGPSKYF 168
                                                                                                                                                                                                                                                 57 KLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHFGNH 110
                                                                                                                                                                                                                                                                                                                              123 FDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE 182
                                                                                                                                                                                   1 QOPPDPSQLHRSS-LVKKMLQNIYFLYEGDPVTHENVKSVPQLLSHHLIYNVSG---PNYD 56
                                                                                                                                                                                                      3 QPDPMPDDLHKSSEPTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKRLKNYD 62
                                                                                                                    Query Match
Best Local Similarity 47.2%; Pred. No. 1.9e-32;
Matches 111; Conservative 43; Mismatches 67; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                       239 AA; 27612 MW; BB7BD6204731ED24 CRC64;
Pfam; PF01123; Stap_Strp_toxin; 1.
PRIMTS, PR00279; Btap_Strp_tox_C; 1.
PROSITE; P800279; BTAPH_STREP_TOXIN_1; 1.
PROSITE; P800278; STAPH_STREP_TOXIN_1; 1.
NON TER
SEQUENCE 239 AA; 27612 MW; BB7BD620473
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Search completed: May 7, 2004, 12:09:08 Job time : 49 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
              Copyright
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- protein search, using sw model OM protein 7, 2004, 12:00:52 ; Search time 60 Seconds (without alignments) 1040.717 Million cell updates/sec Мау Run on:

US-10-625-221-14
1178
1 QODPDPSQLHRSSLVKNLQN......KDNETLDSNTSQIEVYLTTK 221 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04:* 1: geneseqp1980s:* 2: geneseqp1990s:*

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tion	7 Streptoco					_	4		m					7				11 Amino aci	39 Streptoco			1 Streptoco	33 Streptoco		
Description	Aaw12097	Aaw59780	Aaw12154	Aaw12146	Aaw12150	Aaw1214	Aab6734	Aaw12148	Aaw1215	Aaw12151	Aaw12152	Abu62460	Aar13209	Aar4501	Abb76240	Aaw12149	Aaw59798	Aaw59781	Aay70109	Abb79508	Abu1008	Abu62331	Aae3768	Aaw1214	Abu62334
ΔI	AAW12097	AAW59780	AAW12154	AAW12146	AAW12150	AAW12147	AAB67344	AAW12148	AAW12153	AAW12151	AAW12152	ABU62460	AAR13209	AAR45017	ABB76240	AAW12149	AAW59798	AAW59781	AAY70109	ABB79508	ABU10088	ABU62331	AAE37683	AAW12145	ABU62334
BB	N	7			N																				7
Length	251	251	251	251	251	251	221	251	251	251	251	251	221	221	221	251	251	251	251	251	251	251	251	250	220
% Query Match	100.0	100.0	99.7	99.7	9.66	99.6	99.2	99.2	99.2	99.5	99.2	98.8	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.3	95.2
Score	1178	1178	1175	1174	1173	1173	1169	1169	1168	1168	1168	1164	1163	1163	1163	1163	1163	1163	1163	1163	1163	1163	1163	1158.5	-
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Aae37687 Streptoco Abu62335 SPEa L42R Aae37684 Streptoco	686	Syn		Aay92319 Plant-opt Abb79503 Staphyloc Abu10083 Staphyloc		Abb/623/ Staphyloc Abu62453 S. aureus Aar13206 Staphyloc	Aar45014 Staphyloc
AAE37687 ABU62335 AAE37684	AAE37689 AAE37688 AAE37691	ABU79074 AAW64647	AAW06737 ABU79069	AAY92319 ABB79503 ABU10083	ABU62326 AAE37678	ABB76237 ABU62453 AAR13206	AAR45014
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220 468 468	220 220 420 820	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	255 255 266 266 266 266 266 266 266 266	266 266 266	266 266	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	239
95.2	94.8 94.7 7	83.1 48.7	2 4 4 6 8 8 6 6 6	48.4 47.8 47.8		4.4.4 7.7.7 7.0.0	
1122	1117	978.5 574	572	570 563 563	563	200 200 200 200 200	559
26 27 8	1 0 0 c	10 m c	9 B C	3.88 9.89 9.99	4 4 0 L	4 4 4 5 0 0 0	5.45

## ALIGNMENTS

AAW12097 standard; protein; 251 AA. RESULT 1

AAW12097;

(first entry) 04-NOV-1997 Streptococcus pyogenes Streptococcal toxin A.

Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.

Streptococcus pyogenes.

1. .30 /label=_sig_peptide 31. .251 /label= mat_peptide Location/Qualifiers Key Peptide Peptide 

07-JUN-1996; 19-DEC-1996.

WO9640930-A1

95US-00480261. 07-JUN-1995;

96WO-US010252.

(MINU ) UNIV MINNESOTA.

Schlievert PM, Roggiani M,

Stoehr J, Ohlendorf D;

WPI; 1997-099936/09. N-PSDB; AAW12097. Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Disclosure; Page 77-79; 102pp; English.

The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE -A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce

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Gaps

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Length 251; Indels 120 150 180 210

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toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies that neutralise wild type SPE-A toxin activity. The toxins can be used in acciding and therapeutics to generate a protective immune response against streptococcal infection. They can be used to protect against the development of streptococcal toxic shock syndrome (STSS). In addition, the toxins can be used for treating animals with symptoms of streptococcal infection or STSS and in methods for stimulating T cell proliferation and in the treatment of cancer. In particular they can be used for treating T cell lymphomas, and ovarian and uterine cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcal; toxin A, SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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                                                                                                                                                                                                                                                                                                                                                                                                1 QODDDPSQLHRSSLVKNLQNIYFLYBGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPWFDFFPEPEPEPEXXXLMIYKDNETLDSNTSOIEVYLTTK 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "wild type Ser replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlendorf D;
                                                                                                                                                                                                                        Ouery Match
100.0%; Score 1178; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.3e-101;
Matches 221; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .. .30
/label= sig_peptide
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/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW12154 standard; protein; 251
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Synthetic.
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                                                                                                                                                                                             Sequence 251 AA;
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                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210
                                                                                                                                                                                                                                                                                                                                                                                ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSIDGIOSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                         90
                         and streptococcal toxic shock syndrome (STSS). The mutant SPB-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibictic therapy. The mutant SPB-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPB-A can be selectively toxic to T cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the Streptococcus pyogenes exotoxin. (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least as change and is nonlethal compared with a protein to wild type SPE-A
         to protect animals against wild type SPE-A and to treat cancer
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                                                                                                                                                                                                                                                                                                                                 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention treatment of streptococcal infection or toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A; wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer; streptococcal toxic shock syndrome; STSS; T cell lymphoma;
                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                            100.0%; Score 1178; DB 2; Length 251; 100.0%; Pred. No. 8.3e-101; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of Streptococcus pyogenes exotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFWFDFFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 251
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                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 221; Conservative
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                                                                                                                                                                                               Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uterine cancer.
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                                                                                                                                                                                                                                Query Match
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WPI; 1997-099936/09

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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal animals against which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVX 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcal, toxin A, SPE-A, non-lethal, mutant, production, vaccine, protection, treatment, cancer, neutralising antibody, streptococcal toxic shock syndrome, SES, symptom, amelioration, fever, hypotension, group A streptococcal infection, myositis, fascitis, liver damage, T cell; lymphoma, ovarian; uterine.
              Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QODPDPSQLHRSSLVKXLQNIYFLYEGDPVTHENVKSVDQLLSHHLIXNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 1175; DB 2; Length 251; 99.5%; Pred. No. 1.6e-100; 1.ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "wild type Lys replaced by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWFDFFPEPEFFQAKYLMIYKDNETLDSNTSQIEVYLTTK 251
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/label=_sig_peptide
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                                                                                              Example 4; Page; 102pp; English
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Best Local Similarity 99.5
Matches 220; Conservative
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19-DEC-1996

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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STES). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                       Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
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                                                                                                           Ohlendorf D;
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                                                                                                           Stoehr J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW12150 standard; protein; 251 AA.
                                                                                                                                                                                                                                        Claim 5; Page; 102pp; English
             96WO-US010252.
                                              95US-00480261
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                                                                           (MINU ) UNIV MINNESOTA
                                                                                                                                        WPI; 1997-099936/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 251 AA;
                                                                                                           Schlievert PM,
                                              07-JUN-1995;
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPB-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                      Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 251;
                                                                                    /note= "wild type Lys replaced by Asn"
                                                                                                                                                                                                                                                                                                   Ohlendorf D;
                                                                                                                                                                                                                                                                                                   Stoehr J,
 label sig_peptide
                              31. .251 _____/label= mat_peptide
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                                                                                                                                                                                                                                                               (MINU ) UNIV MINNESOTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 251 AA;
                                                                     Misc-difference
                                                                                                                                                                                             07-JUN-1996;
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                                                                                                                          WO9640930-A1
                                                                                                                                                           19-DEC-1996
                                   Peptide
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ö VSIDGIQSLSFDIETINKGMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIFKNKE 210 ELKNOEMATLFKOKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120 ELKNOEMATLFKOKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLBIPKKIVVK 150 VSIDGIQSLSFDIETNKOMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180 9 90 QODPDPSQLHRSSLVNNLQNIYFLYEGDPVIHENVKSVDQLLSHHLIYNVSGPNYDKLKT QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT Gaps ö 1; Indels SFWFDFFPEFFTQSKYLMIYKONETLDSNTSQIEVYLITK 221 SFWPDFFPEPEFETQSKYLMIYKDNETLDSNTSQIEVYLTTK 251 Score 1173; DB 2; Pred. No. 2.4e-100; 0; Mismatches 1; Query Match
Best Local Similarity 99.5%;
Matches 220; Conservative ( Н 91 181 31 61 121 151 a ઠે g g g ò à

Streptococcus pyogenes Streptococcal toxin A mutant Asn20Asp 04-NOV-1997 AAW12147 RESULT 6
AAW12147
ID AAW1
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AC AAW:
XX
DT 04-1
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AAW12147 standard; protein; 251 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A is eacher in Trial thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
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Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
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                                                                                                                                                                                                                                                                                      /note= "wild type Asn replaced by Asp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%; Score 1173; DB 2;
99.5%; Pred. No. 2.4e-100;
iive 1; Mismatches 0;
                                                                                                                                                                                             1. .30
/label= sig_peptide
31. .251
/label= mat_peptide
                                                                                                                                                                         Location/Qualifiers
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nes 220; Conservative
                                                                                                                    Streptococcus pyogenes
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                                                                                                                                                                                                                                                                    disc-difference
                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1996;
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                      Streptococcal; toxin A, SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrame; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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                                                                                                    Streptococcus pyogenes Streptococcal toxin A mutant N20D/K157E.
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99.2%; Score 1169; DB 2;
Best Local Similarity 99.1%; Pred. No. 5.7e-100;
Matches 219; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      . .30
label=_sig_peptide
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           /label= mat_peptide
AAW12148 standard; protein; 251 AA.
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1995;
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                                                                      04-NOV-1997
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                                                                                                                                                                                                                                                                     Synthetic
                                   AAW12148;
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   Sold xol xol xol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a tumour cell capable of stimulating antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSIDGIQSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QODPDPSQLHRSSLVKWLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYNVSGPNYDKLKT, 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor cell capable of stimulating antitumor immune reactivity in vitro o in vivo comprises exogenous nucleic acids encoding a superantigen and a costimulatory molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 SFWFDFFPEFFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1169; DB 4;
Pred. No. 4.8e-100;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anticancer immune response in vivo or ex vivo
                                                                                                                                            Streptococcus pyrogenes toxin A protein.
                                                                                                                                                                                Tumour; cancer; immune; enterotoxin
                                   AAB67344 standard; peptide; 221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 2; 16pp; English
                                                                                                                                                                                                                                                                                                                                                        89US-00416530.
90US-00466577.
91WO-US000442.
92US-00891718.
94US-00189424.
95US-00491746.
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Best Local Similarity 99.5
Matches 220; Conservative
                                                                                                                                                                                                                  Streptococcus pyogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1992;
02-MAR-1993;
31-JAN-1994;
                                                                                                                                                                                                                                                                                                                        30-OCT-1998;
                                                                                                                                                                                                                                                    US6180097-B1
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                                                                                                          23-APR-2001
                                                                                                                                                                                                                                                                                      30-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                          03-0CT-198
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                                                                       AAB67344;
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AAW12148
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Gaps .; 0

Indels

Pred. No. 7e-100; ); Mismatches 1;

Best Local Similarity 99.5%; Pre Matches 220; Conservative 0;

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9 90 61 BLKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120

31 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT

91 BLKNQEMATLFXDKNVDIYGVEYYHLCYLSENAERSACIYGGVTNHFGNHLEIPKKIVVK 121 VSIDGIQSLSFDIETNKKANTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE

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151 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKXETGYIKFIPKNKE 210

221

211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK

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AAW12151 standard; protein; 251

RESULT 10

AAW1215

AAW12151;

150 180

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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
VSIDGIQSLSFDIETNKKANTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                              Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes Streptococcal toxin A mutant Cy890Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ser"
                                                                                                                                                             211 SFWFDFFFEFFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                              SEWFDFFFFFFFFFFFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlendorf
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/label=_sig_peptide
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/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                        AAW12153 standard; protein; 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to trast cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                  Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                       Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.
                                                                                                                                                                                                                                                                                                                                    /note= "wild type Cys replaced by Ser"
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/label= sig_peptide
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/label= mat_peptide
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                                           (first entry)
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                                           04-NOV-1997
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                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                           Peptide
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Length 251;

DB 2;

99.2%; Score 1168;

Sequence 251 AA;

Query Match

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23/10/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 VSIDGIQSLSFDIETNKKKVVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPB-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPB-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPB-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                             31 QODPDPSQLHRSSLVKNLQNIYFLYEGDDVTHENVKSVDQLLSHHLIYNVSGPNYDKLXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                 1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                    tch 99.2%; Score 1168; DB 2; al Similarity 99.5%; Pred. No. 7e-100; 220; Conservative 0; Mismatches 1;
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/label=_gig_peptide
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/label= mat_peptide
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Synthetic.
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Best Local Similarity
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                                                                                                                                                                                                     Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 VSIDGIQSLSPDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                     The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                       90
                                                                                                                                                                                                                                                                                                                                                                                       QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSASIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                           QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPEa; streptococcus pyrogenic enterotoxin a; mutant; vaccine; mutein; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                             Length 251;
                                                                                                                                                                                                                                                                                             Score 1168; DB 2; Length 2
Pred. No. 7e-100;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEWFDFFPEPFTQSKYLMIYKONETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyrogenic toxin a L42A mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31. .251
/label= Mature_SPEa_L42R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .30
label= Signal_peptide
streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU62460 standard; protein; 251 AA
                              Example 4; Page; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00882431.
98US-00144776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003036644-A1
                                                                                                                                                                                                                                                                  Sequence 251 AA;
                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi]
Matches 220; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-1997;
01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                              31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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WO9110680-A.

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VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELKNOEMATLEKOKNVOIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSIDGIQSLSFDIETNKGAVTAQELDYKVRKYLTDNKQLYINGPSKYETGYIKFIP<u>KNKE 180</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPE A can be used for tumouricidal treatment, esp. with a haemolysin. Synthetic polypeptides having structural homology to Streptococcal pyrogenic exotoxins are claimed, provided the homology includes etatistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See AAR13203-R13211. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                           Treating cancer with enterotoxin from Staphylococcus aureus - administered by IV injection, having same tumoricidal activity Staphylococcal protein A without potential toxic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1163; DB 2; Length 221;
Pred. No. 1.7e-99;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcal enterotoxin, SE; cancer; tumouricidal agent;
autoimmune disease; toxicity; Protein A; perfusion system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR45017 standard; protein; 221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcal enterotoxin SPE A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-US005213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 99.1%;
Matches 219; Conservative (
                                                                                         90US-00466577
                                                                                                                                       90US-00466577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
                                                                                                                                                                                                                                                                                   WPI; 1991-237984/32.
                                                                                                                                                                                       (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9324136-A1
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                                                                                           17-JAN-1990;
                                                                                                                                       17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
08-JUN-1994
                                             25-JUL-1991
                                                                                                                                                                                                                                     Terman DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR45017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                              The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant by construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered 1857-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen toxin peptide, diagnosing superantigen toxin period immunogenic response resulting in the protection infection, a vaccine (comprising an altered superantigen toxin) of a mammal against superantigen-response resulting in the protection, of a mammal against superantigen-associated bacterial infection, an infection and individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 Superantigen toxin and an antibody which recognises altered TSST-1 Superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterctoxin a and b (SPEa and SPED). The superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 SPED). The superantigen toxin and an antibody which recognises altered TSST-1 SPED). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the L42A (with reference to the mature protein) cuttent of SPEa not sequence is not shown in the specification but was created by the indexer using the wild-type sequence specification but was created by the indexer using the wild-type sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 VSÍDGÍQSLSFDIETNKKAVTAQELDYKVRKYLÍDNKQLYTNGPSKYETGYIKFIPKAKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                             New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 ÓÓDÞÓÞSÓLHRSSLVKKLÓNÍÝFLYBGDÞVTHBNVKSVDÓLASHDLÍYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIXNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 SFWFDFFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1164; DB 7;
Pred. No. 1.6e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%; Scor.
99.1%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13209 standard; protein; 221 AA
                                                                                                                                                                                                                                            Example 13; Page; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.13
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                            WPI; 2003-492125/46.
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                            (ULRI/) ULRICH R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2003
15-OCT-1991
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Gaps

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treating cancer

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The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SE8) which may be used in the methods of the invention for treating cancer in a patient. These SE8, and homologues of them, can be used as tumouricidal apents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administered by i.v. injection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                              61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGYTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                     1 QODPDPSQLHRSSLVKNLQNIYPLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                         1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exotoxin A; SPE A; superantigen; antigen; tumour; cancer; antitumour;
                                                                                                                                                                                                                                                                                                                Query Match

98.7%; Score 1163; DB 2; Length 221;
Best Local Similarity 99.1%; Pred. No. 1.7e-99;
Matches 219; Conservative 0; Mismatches 2; Indels
                                                                                                      and homologues - for auto-immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEWFDFFPEPFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFWFDLFPEPEFTQSKYLMIXKONETLDSNTSQIEVYLTTK 221
                                                                                                        Use of staphylococcal enterotoxin(s) in a patient or for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus pyogenes exotoxin A.
                                                                                                                                                  Disclosure; Fig 1; 90pp; English
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90US-00466577.
91WO-US000342.
92US-008917118.
94US-00189424.
95US-00491746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes
                                                    Terman DS, Stone JL;
                                                                            WPI; 1993-405418/50.
          (TERM/) TERMAN D S. (STON/) STONE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002051765-A1
                                                                                                                       in a patient or
                                                                                                                                                                                                                                                                                           Sequence 221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1991;
01-JUN-1992;
02-MAR-1993;
31-JAN-1994;
19-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2002
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Gaps .; 0

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My 65 FMMS
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C patient to induce an in vivo therapeutic, tumouricidal reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACTYGGGVTNHEGNHLEIPKKIVVK 120
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                                                                                                       need for e.g. radiotherapy, cells sensitized to a growing
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                                                                                                         Reagent for treating cancer without the comprises a specific V beta subset of T tumor and stimulated with superantigens.
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                                                                                                                                                                                    Disclosure; Fig 2; 17pp; English
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Best Local Similarity 99.1
Matches 219; Conservative
                                                                     WPI; 2002-415198/44
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 1200)

SS ii, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Brail: seqref@agenoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSOCAP008BE02QPI.

Location/Qualifiers

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               EX443774 EX443774
EX44626 EX46286
AL565455 AL565455
AL565455 AL565455
AL663921 Drosophil
AL063706 Drosophil
AL063706 Drosophil
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AL536104 AL536104
EX439779 EX458623
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EX439779 EX458623
CG753083 P048-1-C0
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CG753084 P048-3-D0
AL085149 Tetracochil
EX43775 EX415076
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EX415070 Drosophil
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BX446296
AL566455
CNS00396
CNS00396
CNS002VL
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CG753083
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CG750135
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CNS00EVL
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BX456575
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BX420717
CNS003BD
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BX437758 BX437758
CC253231 CH261-180
AL063921 Drosophil
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              GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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CC253231
CNS0039G
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                                                              using sw model
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/tissue type="HITMUS"
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/.organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="Taxon:9666"
/clone="SCOCAPOORYBO!"
/fissue_type="THYMUS"
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/note="Vector: PCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, the Not I and Cloned into the Not I and Cloned into Library was not normalized."
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BX437758 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP008YB01
5-PRIME, mRNA sequence.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
1 (Ji, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 19 19106 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Conteact : Feng Liang Email : filangelifetch.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPOOSCAOLOGPI.
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03-JUN-1999
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473 AACTICAICATCTCTCACTITITCGTGTGGTAACACACAIAAICAAATATCTTTCGGTTTTT 532
                                                                                             711 ATATACAATTTTATTCTATTTATAGTTAGCTATTTTTTCATTGTTAGTAATATTGGTGAA
                                                                                                                                                                                                                                                                                                                                                           GGGCCAAATTATGATAAAATTAAAAACTGAACTTAAGAACCAAGAGATGGCAACTTTATTT
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                               533 ACGCACTATCGCTACTGTGTCACCTAAAATATACCCCTTATCAATCGCTTCTTTAAACTC
                                                                                                                              ATTGTTTTTTTTTTTTTTTTAATAAATT--ATTAATATATAAGTTAATGTTTTTTAAAA
                                                                                                                                                                                                                                                                                            891 CTAACAATCTCGCAAGAGGTATTTGCTCAACAAGACCCCGGATCCAAGCCAACTTCACAGA
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                                                                                                                                                                                                                                                             TT-----TYWWAAWATTYTTTTTTTMWAAAAAAAAAAAATTTTTYYYMAAAAAAAA 439
                                                                                                                                                                                                                                                                                                                 438 YMHWWWTWTTWAWWWHTTYAHAACHYMYTCYCTYWWAAAAAAAAAATCTHTWTWTHHHHHW 379
                                                                613
ТААААААМТТУСТТСТСҮГТТТСГИМТИТТГИАМАМАТҮҮМҮГТССТИТИТАММАМАМ 673
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galius gallus (chicken)
Gallus gallus
Kararyota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1277)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                    672 ИМТАТМТАУУТСНУИММАААСААМАААААААААААААААААМИМИНСУТТИАМААААА
                                                                                               AAAAAGTATTGAAGAAAATGGTATTTTTTTTTTTAGTGACATTTCTTGGACTAACAATCT
                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center
Washington University School of Medicine
Small: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: RMI TACGACTCACTATAGGGAGA
Class: BAC ends
High quality sequence start: 24
High quality sequence stop: 85.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
/cell_line="UCD001, inbred 256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
/mol type="genomic DNA"
/strain="Red Jungle Fow1"
/db xref="taxon:9031"
/clone="CH261-180N11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1277 bp
CH261-180N11 RM1.1 CH261 Gallus
genomic survey sequence.
CC253231
                                                                                                                                                                                                                                                                                                                                                             ATGATAAATTAAAACTGAACT 1102
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VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
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CC253231
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1200 bp mRNA linear EST 22-MAY-2003
BX437739 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP008YG24
BX437739
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/clone lib="Homo saplens THYMUS"
/clone lib="Wector: PCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI and cloned into
the Not I and clone strand obla was digested with Not I and cloned into
the Not I and ECRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Genoscope - Centra National de Sequencage
Genoscope - Centra National de Sequencage
BP 191 91006 ENRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 534.r For
more information about this cluster, see
http://www.genoscope.cns.fr,
cgi.bin/cluster.cgi?seq-CSOCAP008BD12NP1&cluster=534.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fullbengh.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP008BD12NP1.
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                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 1200)
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GGTAACACATAATCAAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGTCACAAA
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4.9%; Score 91.6; DB 13; Length 1200;
Best Local Similarity 37.4%; Pred. No. 5.3e-05;
Matches 301; Conservative 110; Mismatches 387; Indels 6;
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/clone="CSOCAP008YG24"
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Homo sapiens
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the brosophila melanogaster genome using these BACs. For further information please see http://www.fruitffy.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and haron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridizathion from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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     of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
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5.1%; Score 93.8; DB 29;
Best Local Similarity 18.3%; Pred. No. 2.5e-05;
Matches 123; Conservative 287; Mismatches 261;
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'organism="Drosophila mel'

mol type="genomic DNA"

'db_xref="taxon:727"

'clone="BACROSK10"

/clone=lb="RPCI-98"

/note="end: TET3"
           11y), genomic survey sequence. AL063921
                                                                                   AL063921.1 GI:4941778
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EST 15-MAY-2003
                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
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/note="lip="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="lip="Homo sapiens PlaceNYA COT 25-NORMALIZED"
/note="lip="temo cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORI 6 vector. Library was normalized.
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Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com Uhttp://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI002BC06NP1. Location/Qualifiers
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4.9%; Score 91.4; DB 13;
Best Local Similarity 31.4%; Pred. No. 5.7e-05;
Matches 217; Conservative 175; Mismatches 290;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                              CTACCGTCACAACTTCATCTCTCACTTTTTCGTGTGGTAACACATAATCAAATAT--
                                                                                                                                          -CTTTCCGTTTTTACGCACTATCGCTACTGTGTCACCTAAAATATACCCCTTATCAATCG
                                                                                                                                                                                                                                                                                            GATAAAAATAACTATTGTTTTTTTTTTTTTTATAAAATTATTAATAAAGTTAAT
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BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.ons.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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Matches 408; Conserv
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Genoscope - Centra National de Sequencage
Genoscope - Centra Verance
BP 191 90006 EVRY cedex - France
BP 191 90006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Inhitzogen. This sequence belongs to sequence cluster 7885.f For
more information about this cluster, see
http://www.genoscope.cns.fr,
cgi.bin/cluster.cgi?seq-CSODH007DC06QP1&cluster=7885.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://tullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODH007DC06QP1.
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BX443774 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA
clone CSODH007YF12 5-PRIME, mRNA sequence.
BX443774
                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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4.9%; Score 91.2; DB 13; Length 1201;
Best Local Similarity 40.9%; Pred. No. 6.1e-05;
Matches 255; Conservative 68; Mismatches 294; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                          BX443774.1 GI:30772178
                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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CH261-167M9_Sp6.1 CH261 Gallus gallus genomic clone CH261-167M9,
genomic survey sequence.
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1001 CCCTGTTACTCACGAGAATGTGAAATCTGTTGATCAACTTTTATCTCACCATTTAATATA 1060
                                                                                            1061 TANTGITTCAGGGCCAAATTATGATAAATTAAAAACTGAACTTAAGAACCAAGAGATGGC 1120
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                                           731 รานนำนำนานรานนานนานานา-ไฟน่านพพทานน่านานานานานานานานนาน 673
                                                                                                                                                                                                                                          /cell line="UCD001, inbred 256"
/clone lib="CH261"
/note="Vector: pTARBAC2.1; Site 1: EcoR1; Site_2: EcoR1;
CH261 Female Chicken library - For library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Ballus.

1 (Dases 1 to 1202)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
Contact: Richard K. Wilson
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Pred. No. 8.7e-05;
0; Mismatches 498;
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Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="KR61-167M9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 30
High quality sequence stop: 105.
Location/Qualifiers
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44.5%; Pred
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CC262481.1 GI:30607397
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Gallus gallus
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BX436282 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YC01
BX436282 EFPRIME, mRNA sequence.
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                                                              AGAACCCAGATATAAAATGGAGGAATATTAATGGAAAAACAATAAAAAAGTATTGAAGAAA 857
                                                                                  AGCTATITITICATIGITAGIAATATIGGTGAATIGIAATAACCTITITAAAICTAGAGG 797
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Catarrhini; Hominidae; Homo.
                                                                                                                                                    CAACAAGACCCCGATCCAAGCCAACTTCACAGATCTAGTTTAGTTAAAAACCTTCAAAAT
                                                                                                                                                                        754 TTAAATATATATATATATATATAAAATTAAAAAATTTTATTAATAATAAATTAANAATAA
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                                         ATGGTATTTTTTTTAGTGACATTTCTTGGACTAACAATCTCGCAAGAGGTATTTGCT
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Genoscope - Centre National de Sequencage
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Mammalia; Butheria; Primates;
1 (bases 1 to 1124)
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO01AB01QP1.
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Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                     1064 TGTTTCAGGGCCAAATTATGATAAATTAAAACTGAACTTAAGAACCAAGAGAGATGGCAAC 1123
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

1 'I. W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                    1124 TITATITIAAGGATAAAACGITGATATITIATGGTGTAGAATATTACCATCTCTGT-TATT
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Contact: Genoscope.
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Enail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com U
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : XCL0BB001ZA03FF1.
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4.8%; Score 89.6; DB 13;
Best Local Similarity 35.8%; Pred. No. 0.00011;
Matches 194; Conservative 87; Mismatches 261;
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                                                     AL565455 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone CSODF005Y018 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Best Local Similarity 32.4%; Pred. No. 0.0001;
Matches 243; Conservative 135; Mismatches 372; Indels 1
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was primed with a NotI-oligo(dT) primer. Five prime end
was primed, double-srrand cDNA was digested with Not I and
cloned into the Not I and BcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                          167 TABATTCAATCTAATTACTAACAAGCAACTAGATTGACAACTAATTCTCAACAAAGG
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                                                                                                                                                                                                                                                                                                                                                               Length 1201;
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                                                                                                                                                                                                                        ch 4.8%; Score 88.8; DB 9; Similarity 34.2%; Pred. No. 0.00014; 247; Conservative 123; Mismatches 350;
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1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12916848.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EWRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: seqrefogenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF005BH09NP1&cluster=9232.f. Contact
Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF005BH09NP1.
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                                                                           TGACAACTCTTCAATTATTTTTTTTGTCTACTCAAAGTTTTCTTCATTTGATATAGTCTAA
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                             /organism="Homo sapiens"
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GSS 03-JUN-1999

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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4.8%; Score 88.4; DB 29;
Best Local Similarity 20.3%; Pred. No. 0.00017;
Matches 146; Conservative 295; Mismatches 269;
                                                                                                         Drosophila melanogaster (fruit fly)
                    fly), genomic survey sequence. AL063921
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                                                                      AL063921.1 GI:4941778 GSS.
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Direct Submission

Submitted (102-UJW-1999) Genoscope - Centre National de Sequencage:

By 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila (Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org the BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the ECORI digestion of Drosophila DNA provided by the BDGP from the ECORI digestion of the Sp. the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
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Similarity 34.9%; Pred. No. 0.00021;
11; Conservative 122; Mismatches 284; Indels
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/clone lib="RRC19B3"
/note="end : T7"
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1 (Dasses 1 to 1201)

2 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

1 Unpublished (2001)

2 On Feb 13, 2001 this sequence version replaced gi:12799597.

Contact: Genoscope Genoscope - Centre National de Sequencage

BP 191 91006 ENRY cedex - France

Email: seqref@genoscope.cns.fr Library was constructed by Life Technologies, a division of Invirrogen. Contact: Feng Liang Email: fliangelifetech.com URL:

Library was constructed by Life Technologies, a division of Invirrogen. Contact: Feng Liang Email: fliangelifetech.com URL:

Faradas Avenue Genoscope sequence ID: CSODF022BB09QP1.
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TTWWTATWTWTTTTWTTTWWTATWTATATATATAAWTAATTWWTWTATATWTAWWTA 1042
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                              CACTATCGCTACTGTGACCTAAAATATACCCCTTATCAATCGCTTCTTTAAACTCATC
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.one="CS0DF022YC18"
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May 8, 2004, 10:40:02; Search time 7000 Seconds (without alignments) 11461.137 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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	unknown. Unclassified.  1 (bases 1 to 1851)  2 Chlievert, P.M., Roggiani, M., Stoehr, J. and Ohlendorf, D. Schlievert, P.M., Roggiani, M., Stoehr, J. and Ohlendorf, D. Mutants of streptococcal toxin a and methods of use Patent: US 6632441-A 12 14-OCT-2003;  Location/Qualifiers
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                           TGABARTCTGTTGARGACTTTTATCTCACCATTTAATATATATGTTTCAGGGCCAAATT
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1 (bases 1 to 1851)
Schlievert, P.M., Roggiani, M., Stoehr, J. and Ohlendorf, D.
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Location/Qualifiers

1. 1851

/ Organism="unidentified"
//mol_type="genomic DNA"
//db_xref="taxon:32644"

Query Match

Best Local Similarity 100.0%; Score 1851; DB 6; Length 1851;

Best Local Similarity 100.0%; Pred. No. 3.2e-256;

Matches 1851; Conservative 0; Mismatches 0; Indels 0; Gaps
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Mutants of streptococcal toxin A and methods of use Patent: JP 2001505439-A 12 24-APR-2001;
REGENTS OF THE UNIVERSITY OF MINNESOTA
PN JP 2001505439-A/12
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PP 05-DEC-1997 JP 1998525794
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                                                                                    1621 AATTCTTTATTAATGTAAAACGGCTCATTTGATGAGGGGTTTTGTCTTATCTAAGGA
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       AATTCTTTTATTAATGTAAAACCGCTCATTTGATGAGCGGTTTTGTCTTATCTAAAGGA
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99.0%; Score 1832.2; DB 6; Length 1837;
Best Local Similarity 99.8%; Pred. No. 1.6e-253;
Matches 1834; Conservative 0; Mismatches 3; Indels 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAATG 1320
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                                                                  1321 GTAACTGCTCAAGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTA
                                                                                                              TATACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTCATACCTAAGAATAAA
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Patent: WO 03056015-8-15 10-JUL-2003;
U.S. Medical Research Instruce_of_Infectious Diseases (US)
Location/Qualifiers
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| organism="synthetic construct"
| /mol_type="unassigned DNA"
| /db xref="texon:32630"
| /note="streptococcal pyrogenic exotoxin-A mutant"
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98.9%; Score 1830.6; DB 6; Length 1837;
Best Local Similarity 99.8%; Pred. No. 2.7e-253;
Matches 1833; Conservative 0; Mismatches 4; Indels 0;
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Sequence 15 from Patent W003056015.
AX800046.1 GI:37653325
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/protein id="AAC4868.1"
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DKNVDIXQPRYFHLCYLCENABRSACTORYTHBGNHLEIPKKIVVKVSIDGIQSLS
FDIETYNKKNYTAQELDYKVRKXLTDNKQLYTNGPSKXETGYIKFIPKNKESFWFDFFP
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/db_xref="GI:1877428"
/translation="MFHGMNYNSYKANNNLLEIRHLEDIVKYNTIMRDQYKKGSNBYN
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/note="phage attachment site; 96 bp duplication with
/note="phage attachment site; 36 bp duplication with
Streptococcus pyogenes chromosome at bacterial attachment
site, 3, end of serine tRNA gene"
3014. .3015
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                                                                                   940
McShan, W.M., Tang, Y.-F. and Ferretti, J.J.

Direct Submission
Submitted (09-NOV-1995) William M. McShan, Microbiology and
Emmunology, University of Oklahoma Health Sciences Center,
In. Young Blvd., Oklahoma City, Ok 73104, USA
On Mar 12, 1997 this sequence version replaced gi:216177.

Location/Qualifiers
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3597. .4352
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1. .4621.

/organism="Streptococcus pyogenes phage T12"

/mol_type="genomic DNA"

/db xref="taxon:35344"

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1883. .2971
/gene="int"
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codon start=1
trans1_table=11
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1532. .1750
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1597. .4352
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Weeks,C.R. and Ferretti,V.J.
Nucleotide sequence of the type A streptococcal exotoxin
(erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1561 ACCAAGTAACTTTTTGCTTTTTGCCAACCTTACCTACTGCTGGATTTAGAAATTTTATTGC 1620
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McShan, W., Tang, Y.F. and Ferretti, J.J.
McShan, W.M., Tang, Y.F. and Ferretti, J.J.
Bacteriophage T12 of Streptococcus pyogenes integrates into the gene encoding a serine tRNA
Mol. Microbiol. 23 (4), 719-728 (1997)
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                                                                                                                    AAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAAAAAATG
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                TACGGAGGGGTAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT
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U40453.1 G1:1877426
Exthrogenic toxin; type A streptococcal exotoxin.
Streptococcus pyogenes phage T12
Streptococcus pyogenes phage T12
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AGCCAACTICACAGAICTAGITIAAAAACCTICAAAAIATAITITITITIAIGAG
            GGTGACCCCGTTTACTCACAGAATGTGAAATCTGTTGATCAACTTTTATCTCACGATTTA
                                                                       ATATATAATGTTTCAGGGCCAAATTATGATAAATTAAAAACTGAACTTAAGAACCAAGAG
                                                                                3825 AIATAIAAIGITITCAGGGCCAAATIATGAIAAAITAAAAACTGAACTIAAGAACCAAGAG
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                                    GGTGACCCTGTTACTCACGAGAATGTGAAATCTGTTGATCAACTTTTATCTCACCATTTA
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Streptococcus pyogenes MG
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AE014161.1 GI:21905010
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     /gene="speA"
/note="butative"
3687. -4349
/gene="speA"
/product="erythrogenic toxin A"
4426. -4456
/note="putative transcription termination signal"
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                                                                                  90.1%; Score 1668.4; DB 7; Length
Llarity 97.4%; Pred. No. 4e-230;
Conservative 0; Mismatches 36; Indels
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complement(38693. .>57506)
complement(38693. .>57506)
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/db_xref="taxon:198842"
complement(141. .1073)
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Araqolpkrygslddhildestdaivvasinodhfprakkrallagkryuverpfilts
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vywrrdlekgogovingraylpylekddivsrsyvahfprogosososkujals
ngvlvdifltthleldprelvivgtkrkeldphykkrythatlyrpdgssrsvieatwssd
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Submitted (14-UUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, MT 59840, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of a serotype M3 strain of group A Streptococcus: Phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                        Streptococcus.

1 (bases 1 to 57506)

1 where S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S., Barbian, K.D., Lei, B., Hoff, J.S., Mamarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F., Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)
2 (bases 1 to 57506)
Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S., Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F., Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and
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/db_xref="G1:21905011"
Streptococcus pyogenes MGAS315
Streptococcus pyogenes MGAS315
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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/mol_type="genomic DNA"
/strain="MGAS315"
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protein id="AAM79878.1"
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                                                                                                                                          complement (7995. 1820)

Gene="EpyM3 1277"

complement (7995. 1820)

Gene="EpyM3 1277"

complement (7995. 1820)

Gene="EpyM3 1277"

/ note="best non-GAS blastp hit; gb|AAK74720.1| (AE007366)

/ protestical protein [Streptococcus pneumoniae TIGR4]"

/ codon start=1

/ trans1 table=11

/ protein id="AAM79884.1"

/ db xref="GI:21905018"

/ trans1ation="MAKGKNRKALKLEMKRNGLLKKAGQVFDXAVESVETAVDXTIS

AGKNLVEKGSGTVENLTARSKRRLTLDERFAGGPVVAGIRSDLVETLYAEGIHSAQAFKE

WTEKDLLALKGIGPATVKKLVENGASFKK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="best blastp hit: gb|AAX34362.1| (AE006589) putative chorismate mutase [Streptococcus pyogenes Ml GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="msyekeflkdfedwyktolqvnolamatsqevaqedderakda
ftryeskldayefllgkfdnykngkafhdvpdelfgarhy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AE008428)
R6] "
    hypothetical protein [Streptococcus pneumoniae"
                                                                                                                       translation="MACKLGFTLEANARDRKDVQGRRCGDMRFGLLRSEWEEQKQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITICITATITITATAAAATTATTAATATAAAGTTAAIGTTITITAAAATATATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 TCATTIGATATAGICTAATTCCACCATCACTTCTTCCACTCTCTCCTACCGTCAACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                  // Codon start=1
/ canol_ment(8311...8865)
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/ note="best non-GAS blastp hit: gb|AAK99291.1|
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/ codon start=1
/ transl_table=11
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                            /codon_start=1
/transl_table=11
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/db_xref="G1:21905017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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/db_xref="G1:21905020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.0%; Score 1406.6; DB 1; Best Local Similarity 99.3%; Pred. No. 7.5e-193; Matches 1423; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: SpyM3_1279"
9044. .9796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1732. .8802
product="tRNA-Thr"
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/gene="aroA.2"
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/protein id="BAC63382.1"
/db_xref="G1:28810445"
/db_xref="G1:28810445"
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LPRRVTGTSAROQRKYTTAIKRARVMALMPYVNED"
/complement(3217, .3873)
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GIMTFFNTNATVTGLISLLALGFGGGASMYATYYFIYRHLGKDKSLRPSWFKIIAALS
LAMLIWIALYSATAFLPTSLNPQLPPLALLIIGGVSLALRYYLORKYNIQNTMSPVNK
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EADPINCYIWRQPAENLANWAKKGALIGYTGRIQTRNYENQGGGRVYYTEVVADNFQM
LESRATREGGSTGSFNGGFNNNTSSSNSYSAPAQQTPNFGRDDSPFGNSNPMDISDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2845. .3084
//gene="SP80287"
//gene="slimilar to GB:AAK34551.1 (AE006609) percent
identity 100 in 79 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to GB:AAL98396.1 (AE010095) percent
dentity 100 in 218 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2189. .2680

2189. .2680

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/gene="SP80286"

/note="similar to GB:AAK34552.1 (AE006609) percent conductry 100 in 163 aa" (codon_terat=1
                                                                                                                                                                                                     note="similar to GB:AAK34553.1 (AE006609) percent
identity 100 in 96 aa"
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/transl_table=11
/product="putative single |
associated)"
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/trans1_table=11
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/gene="SP80288"
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                                                                                                              1877. .2167
/gene="SP80285"
1877. .2167
/gene="SP80285"
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/gene="SPs0287"
2845. .3084
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YIWWSEIMGOOTOVNTVIPYYKRFLEMPPOINDLABABEBGLIKAWRELGYYSRNRNM
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LEFUNYOIGBPKNRKIFQAIMELLIDPDREGDFNQALMDLGTDIESAKTPRPDESPIR
FRAMYLLOTYTGKYPIKNFKKKKKKPKFRAM IQAYVIKNONGOYLLEKNYKRCKLIGGFNSFP
IIETSPLSQULDLENDNGSNPIIMOTONETPEREYQLKFOWTONHFPNIKHTFSHOKM
TIELIEGVVKATDLENAPHLKWVAIEDFSLYPPATFOKKMLETYLKGKNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-MAY-2002) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:kenégen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Pax:81-6-6879-2047)
                                                                                                                                                            BCT 13-JUN-2003 section 2/6.
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This clone was isolated from a patient presenting with toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa,I., Kurokawa,K., Yamashita,A., Nakata,M., Tomiyasu,Y., Okahashi,N., Kawabata,S., Yamazaki,K., Shiba,T., Yasunaga,T., Hayashi,H., Hattori,M. and Hamada,S.
Genome Sequence of an M3 Strain of Streptococcus pyogenes Reveals Large Scale Genomic Rearrangement in Invasive Strains and New Insights into Phage Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 310850)
Yamashita,A., Nakagawa,I., Kurokawa,K., Nakata,M., Tomiyasu,Y.,
Yamazaki,K., Okahashi,N., Kawabata,S., Yasunaga,T., Hattori,M.,
Hayashi,H. and Hamada,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative A/G-specific adenine glycosylase"
/protein_id="BAC63378.1"
/db_xref="G1:28810441"
        40154 CTAACACCAAAATCATAGACAGGAGCTTGTAGCTTAGCAACTATTTATGTC 40206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(89..1243)
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/note="similar to GB:AAL98401.1 (AE010096) percent identity 100 in 374 aa"
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/transl_table=11
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                                                                                                                                                                                                                                                                                           Streptococcus pyogenes SSI-1
Streptococcus pyogenes SSI-1
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
                                                                                                                                                                  DNA linear complete genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Streptococcus pyogenes SSI-1"
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/strain="SSI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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                                                                                                                                                       310850 bp
Streptococcus pyogenes SSI-1 DNA,
AP005142 BA000034
AP005142.1 GI:28810440
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complement(89..1243)
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/gene="SP80284"
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                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                    RESULT 10
AP005142/c
LOCUS
DEFINITION
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TITLE JOURNAL

gene

FEATURES

COMMENT

CDS

REFERENCE AUTHORS

JOURNAL MEDLINE

TITLE

PUBMED

REFERENCE AUTHORS gene

CDS

us-10-625-221-12.rge

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271041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAAAGATAGTCGTTAAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATATGA
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identity of in 942 aa"
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dentity 98 in 357 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1406.6; DB 1; Length
Pred. No. 5.1e-193;
0; Mismatches 9; Indels
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Best Local Similarity 99.3%;
Matches 1423; Conservative
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[Streptococcus pyogenes Ml GAS]"
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   270860 TIAGAAAITITATIGCAAIICTITIAITAATGIAAAACGCICAITIGAHGAGGGGIT 270801
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                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes strain MGAS8232, section 30 of 173 of the complete genome.
AE009982 AE019949
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Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Stundevant,D.E., Ricklefs,S.M.,
Porcella,S.F., Parkins,L.D., Beres,S.E., Campbell,D.S., Smith,T.M.,
Cahang,Q., Kapur,V., Daly,J.A., Vessy,L.G. and Musser,J.M.
Genome sequence and comparative microarray analysis of serotype M18
group, A Streptococcus strains associated with acute rheumatic fever
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Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M.,
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Parlog, Q., Kapur, V., Daly, J.A., Veasy, L.George. and Musser, J.M.
Direct Submission
Submitted (31-JAN-2002) Laboratory of Human Bacterial
Submitted (31-JAN-2002) Laboratories/NIAID/NIH, 903 S. 4th St.,
Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 S. 4th St.,
Hamilton, MT 59840, USA
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/note="best blastp match emb|CAB07986.1| (293946)
N-acetylmuramoyl-b-alanine amidase [bacteriophage Dp-1]"
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protein id="AAL97140.1"
db_xref="GI:19747623"
                                                                                                                     TGTCTTATCTAAAGGAGCTTTACCTCCTAATGCTGCAAAATTTTAAATGTTGGATTTTTG
                                                                                                                                                                                                                                                                  1739 TATTIGICIATIGIATITICATICCATATICCATTITITICGACAGACATCGTGCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                    1799 CTAACACAAAATCATAGACAGGAGCTTGTAGCTTAGCAACTATTTTATCGTC 1851
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Streptococcus pyogenes MGAS8232
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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/mol type="genomic DNA"
/strain="MGAS8232"
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90. .1307
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/note="phi speA"
90. .1307</pre>
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TAATAAGCAACTATAATACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTCAT 1571
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                                                                                                                                                                                                                                                                                                                                   2529 TGGCCTGACTCTCTGGTAACACATAATCAAATATCTTTCCGTTTTTAGGCACTAT
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       Length 11900
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   Score 1225.4; DB Pred. No. 1e-166; 0; Mismatches 31
66.2%;
   Query Match
Best Local Similarity 97.5
Matches 1255; Conservative
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/product="putative aminodeoxychorismate lyase"
/product="putative aminodeoxychorismate lyase"
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/product="putative lyase"
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/dr_xra
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pyogenes M1 GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AE006499)
| [Streptococcus
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/gene="spyMl8 0404"

complement (8258. 9181)
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/note="best blastp match gb|AAK33400.1| (AE006499)
hypothetical protein [Streptococcus pyogenes Ml GAS]"
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putative aminodeoxychorismate lyase [Streptococcus
pygones MI GAS]"
/codon start=1
/transl_table=11
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/gene="gpyM18_0402"
7104. .7634
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/note="best blastp match gb|AAK33399.1| (AE0 putative transcription elongation factor [St pyogenes M1 GAS]"
/codon start=1
/transl_table=11
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/gene="spyM18_0405"
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complement (926
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/transl_table=
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750 ATTGTTAGTAATATTGGGAATTGTAATAACCTTTTTAAATCTAGAGGAGAACCCAGATA 809 	810 TAAAATGGAGGAATATTAATGGAAAACAATAAAAAAGTATTGAAGAAAATGGTATTTTT 869 	GITTIAGIGACATITCTIGGACIAACAAICICGCAAGAGGIATITGCTCAACAAGACCCC	GATCCAACCAACTTCACAGATCTAGTTTAAAAACCTTCAAAATATATTTTCTT 9	TAT	1049 CCRITTARITATRATGITICAGGGCCARATTAIGAIRARATTAARAACIGAACTIRAGAA 1108 	1109 CCAAGAGATGGCAACTTTATTTAAGGATAAAAACGTTGATATTATGGTGTAGAATATTA 1168 	1169 CCATCTCTGTTATTTATGTGAAAATGCAGAAAGGAGTGCATGTATCTACGGAGGGGTAAC 1228 	1229 aaatcatgaaggaatcatttagaaattcctaaaagatagcgttaaagtatcaatcga 1288 	1289 TGGTATCCAAAĞCCTATCATTTGATATTGAAACAAATAAAAATGGTAACTGCTCAAGA 1348 	1349 ATTAGACTATAAAGTTAGAAATATCTTAGAGATAATAAGGAACTATATAGTAATGGAAC 1408 	1409 TTCTAAATATGAAACTGGATATATAAAGTTCATACCTAAGAATAAAGAAAG	1469 IGATTITITCCCIGAACAGAAITITACICAATCIAAATAICTIAIGAIATATAAAGAIAA 1528 	1529 TGAAACGCTTGACTCAAACACAAGCCAAATTGAAGTCTACCTAACAACAAGTAACTTT 1588 	1589 IGCTITIGGCAACCITACCTACTGCTGGATITAGAAAITTITATAGAATTCTITITAA 1648 	9 TGTAAAAACGGCTCATTTGATGAGCGGTTTTGTCTTATCTAAAGGAGCTTTACCTCCTAA 1	896 IGIAAAAA-GGCICAIITGAIGAGGGGITITIGICIIAICIAAAGGAGCITIAGCICCIAA 954		1769 CATTITICGACAGACATC 1786 	
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DD 1570 ACCTAAGAATAAAGAAAGTTTTTGGTTTGATTTTTCCCTGAACCAGAATTTACTCAATC 1511	Qy 1502 TAAATATCTTATGATATAAAGATAATGAAACGCTTGACTCAAACACACAAATTGA 1561 	OY 1562 AGTCTACCTAACAACCAAGTAACTTTTTGCTTTTGGCAACCTTACCTACTGCTGGATTTA 1621	OY 1622 GAAATTTTATTGCAATTCTTTATTAATGTAAAAACCGCTCATTTGATGAGCGGTTTTGT 1681 	Qy 1682 CTTATCTAAAGGAGCTTTACCTCCTAA 1708 	RESULT 12 SPSPEA LOCUS SPSPEA LOCUS SPSPEA 1031 bp DNA linear BCT 21-MAR-1995	fever toxin). X03929 X03929.1 GI:47441	KEYWORDS exotoxin; exotoxin type A; speA gene. SOURCE Streptococcus pyogenes CRGANISM Streptococcus pyogenes Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	Streptococcus.  REFERENCE 1 (bases 1 to 1031) AUTHORS Johnson, b. P., L'Italien, J.J. and Schlievert, P.M. TITLE Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is	related to Staphylococcus aureus enterotoxin B JOURNAL Mol. Genet. 203 (2), 354-356 (1986) MEDLINE 86284313 PUBMED 3526093	FEATURES Location/Qualifiers 1. 1031   source   organism="Streptococcus pyogenes"   mol_type="genomic DNA"			/db_xref="G1:47442" /db_xref="GQA:P08095" /db_xref="SGS-RROT:P08095" /translation="MENNKEVLKRAMVPFVLMKFLGLTILPKGICSTRPKPSQLQRSNL	VKTFKIYIFFMRVTLVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFK DKNVDIYGVEYYHLOYLCENBERSACLYGGVTNHEGNFLEIPKKIVVKVSIDGIQSLS FDIEQIKNGNCSRISYTVRKYLTDNKQLYTNGFSKYETGYIKFIPKNFSFWFDFFPE PRFPOSKYTALYKDNETLDSNYGOJEVYLTTW	sig_peptide 79.168 /note="signal peptide (aa -30 to -1)" mat_peptide 169.828	/product="mature exotox 904920	/note="palindrome por. transcription isc_signal   10031016 /note="palindrome pot. transcription	ORIGIN  Query Match  Query Local Similarity 95.7%; Pred. No. 8.7e-119;  Matches 993; Conservative 0; Mismatches 37; Indels 8; Gaps 7;	

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1488 GAATTTACTCAATCTAAATATCTTATGATATAAAGATAATGAAACGCTTGACTCAAAC 1547
                                                        1548 ACAAGCCAAATTGAAGTCTACCTAACAACCAAGTAA 1583
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/product="type A exotoxin"
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Highly conserved genes and their use to generate probes and primers for detection of microorganisms

Batent: WO 0123604.A 93 05-APR-2001;

Infectio Diagnostic (I.D.I.) INC. (CA)

Location/Qualifiers
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                                                                                                                 Streptococcus pyogenes
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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                               linear
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Corganism="Streptococcus pyogenes"
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                                DNA
                             AX110260 756 bp 1 Sequence 993 from Patent WO0123604.
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AX110260.1 GI:13926552
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Nelson,K.
Direct Submission
Submitted (01-SEP-1991) K. Nelson, Pennsylvania State University,
Inst of Mol Evolutionary Genetics, University Park, PA 16802, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson, K., Schlievert, P.M., Selander, R.K. and Musser, J.M. Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes
J. Exp. Med. 174 (5), 1271-1274 (1991)
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         /isolate="Minnesota"
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/chorensome="bacteriophage e:
/clone="direct PCR fragment"
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/gene="speA"
/gene="speA"
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/product="type A exotoxin"</pre>
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Nelson,K.
Direct Submission
Submitted (01-SEP-1991) K. Nelson, Pennsylvania State University,
Inst of Mol Evolutionary Genetics, University Park, PA 16802, USA
Location/Qualifiers
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J. Exp. Med. 174 (5), 1271-1274 (1991)
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/organism="Streptococcus
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Search completed: May 9, 2004, 10:30:20 Job time : 7007 secs Н

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GenCore version 5.1.6
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(without alignments) 11217.425 Million cell updates/sec

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1851 1 ccatcacgcatcactcatgt......ttagcaactattttatcgtc 1851 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched: 6747726 Notal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* 1: geneseqn1980s:* geneseqn1980s: Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

AAT51716 standard; DNA; 1851 BP. AAT517

AAT51716;

(first entry) 04-NOV-1997 Streptococcus pyogenes Streptococcal toxin A DNA.

Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine; ss.

Streptococcus pyogenes.

/*tag= c /product= "Streptococcal_toxin_A"

%WO-US010252. Location/Qualifiers 828. .1583 sig_peptide mat_peptide Key 

WO9640930-A1

07-JUN-1996; 19-DEC-1996.

95US-00480261. 07-JUN-1995;

(MINU ) UNIV MINNESOTA

Ohlendorf D; Schlievert PM, Roggiani M, Stoehr J,

WPI, 1997-099936/09. P-PSDB; AAW12097. Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Disclosure; Page 77-79; 102pp; English.

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The present sequence encodes Streptococcus pyogenes Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A can seen neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells
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1851 BP: 635 A: 326 C: 248 G: 642 T: 0 U: 0 Other

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SQ Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 U; 0 Other;	Query Match 100.0%; Score 1851; DB 2; Length 1851; Best Local Similarity 100.0%; Pred. No. 4.5e-289; Matches 1851; Conservative 0; Mismatches 0; Indels 0; Gaps	Oy 1 CCATCACGCATCACTCATGACAGCTTATCATAAGCTTACTTTTCGAATCAGG 6	Db 1 CCATCACCACCACCACCACCACCTTATCATCGATAAGCTTACTTTTCGAATCAGG 6	Qy 61 TCTATCCTTGAAACAGGTGCAACATGAGTTTAGGAGATTTACCAGACAACTATGA 1	Db 61 ICTAICCTIGAACAGGIGCAACATAGATTAGGGCATGGAGATTTACCAGACAACTATGA 1		Db 121 ACGIATATACTCACATCACGCAATCGCAATTGACGAACTAAATTCAATCAA		Db 181 İTGİTACTAACAACTAGATTGACAACTAATTCTCAACAAACGTTAATTTAACAACA	QY 241 TICAAGIAACTICCACCAGCICCATCAATGCTTACGTAAGTAATCATAACTTACTAAAA 3		Oy 301 CCTTGTTACATCAAGGTTTTTTCTTTTTGTCTTGTTCATGAGTTACCATAACTTTCTATA 3		Qy 361 TIAITGACAACTAAATTGACAACTCTTCAATTATTTTCTGTCTACTCAAAGTTTTCTCC (		QY 421 ATTIGATATAGICTAATTICACCATCACTICTICCACTCTCTCTACCGTCACACATCAT (		Qy 481 CATCTCACTTTTCGTGTGAACACATAATCAAATATCTTTCCGTTTTTACGCACTA (	Db 481 CAICTCTCACTTTTCGTGTGGTAACACATAATCAAATATCTTTCCGTTTTTACGCACTA (	Qy 541 TCGCTACTGTGACCTAAAATATACCCCTTATCAATCGCTTCTTTAAACTCATCTATAT (		QY 601 ATAACATATTTCATCCTCCTACCTATCTATTCGTAAAAAAAA		OY 661 TITIGITATITIADAATTAATTAATAAAGTTAATGITTTTAAAAATATACAATT		OY 721 TIAITCTAITTAIAGTTAGCTAITTTTTCAITGTTAGTAATAITGGTGAATGTAATAAC O	
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                                                                                                                                                    SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A; wild type; nontoxic; antibody; vactine; immunity; ovarian cancer; streptococcal toxic shock syndrome; STSS; I cell lymphoma; uterine cancer; ss.
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100.0%; Score 1851; DB 2; Length 1851;
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                                                                                                                            Nucleotide sequence of Streptococcus
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                                                1381 ATAATAAGCAACTATATACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTCA
                                                                                                                           TACCTAAGAATAAAGAAAGTTTTTGGTTTTGATTTTTCCCTGAACCAGAATTTACTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       S. pyogenes detection probe #2.
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OUELLETTE M. ROY P H.

(OUEL/) (ROYP/)

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The sequences given in AAT28539-40 represent probes which were used in the method of the invention for the detection of S. pyogenes in a sample. The method comprises using probes and/or amplification primers which are pecific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region by the sample with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of hybridised primers or amplification products as and indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial species. This method may be used to detect commonly encountered bacterial species are didincation and intabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus spidennia, Entercoccus faccalis, Staphylococcus faccanis, Entercoccus faccalis, Staphylococcus spidennia, Entercoccus faccalis, Staphylococcus spidennia, Entercions and with a high percentage of other severe infections including septicaemia, meningitis, pneumonia, conter and pathod may also be used to evaluate a bacterial correstral.
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                                         Method for the detection of bacterial species using probes and primers allows detection and quantification of antibiotic resistant bacteria in patients, the environment and food.
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Pred. No. 1.4e-286;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                Claim 57; Page 92-93; 216pp; English.
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Best Local Similarity 99.9
Matches 1836; Conservative
WPI; 1996-179953/18.
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The invention relates to detecting target bacterial species suspected to be present in a sample, comprising contacting nucleic acids of target be bacterial species with an amplification primer pair derived from a contacting bacterial species with an amplification primer pair derived from a content of bacterial species but ubiquitous for different strains, amplifying the bacterial species but ubiquitous for different strains, amplifying the content and detecting the presence or amount of an amplifying the sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes (ABA76662-CC BAR7684) against the target bacterial species. Specially E.coli, CK.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus, CK.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae, CC A. suspected to be present in a sample which is obtained from human patients, animals, environment or food, and which consists of one or more consist colonies. Oligonaclectide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla(tem), bla(shv), aadB, aac(1, aac(2, aac(3) aac(4), mac(4), varA, varA, varA, varX, varX, satA, aacA-aphD, vat, vag, msrA, sul and/or int (ABA76965-ABA77001) are also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial Streptococcus pyogenes WPI; 2001-615034/71. Bergeron MG, 12-SEP-1995; 12-SEP-1995; 28-JAN-2002 29-JUN-2001 NZ501596-A. 1621 1801 1695 1681 1755 ABA76857; species. QQ 셤 8 8 ò 8 1620 1080 1154 1140 1214 1200 1260 1334 1320 1454 1440 CAACTITIBATCTCACCATTBATATATATGTTTCAGGGCCAAATTATGATAAATTAAAA 1094 GAAAGITITIGGITITGAIIITITICCCIGAACAGAAIITACICAAATGIAAAATAICITAIG 1514 AATATATATTTTTTTTATGAGGGTGACCCTGTTACTCACGAGAATGTGAAATCTGTTGAT 1034 600 674 660 734 AATAAAATTATTAATATAATGTTTTTTAAAATATACAATTTTATTCTATTTATA 720 GITAGCIATITITICALTIGITAGIAATATIGGIGAALTIGIAALAAACCITITITAAATCIAG 794 GTTAGCTATTTTTTCATTGTTAGTAATATTGGGAATTGTAATAAACCTTTTTTAAATCTAG 780 840 914 AAAAIGGTATTTTTTTTTTTTTTTAGTGACATTTCTTGGACTAACAATCTCGCAAGAGGTATTT 900 GCTCAACAAGACCCCGATCCAAGCCAACTTCACAGATCTAGTTTAGTTAAAAACCTTCAA 974 CAACTITIATCICICACGATTAATATATAATGITTCAGGGCCAAATTATGATAAATTAAAA GGTGTAGAATATTACCATCTCTGTTATTTATGTGAAAATGCAGAAAAGGAGTGCATGTATC TATACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTCATACCTAAGAATAAA GABAGTITITIGGITITITITITICCTGAACCAGAAITITACTCAALCTAAATAITATG ATATATAAAGATAATGAAAGGCTTGACTCAAACACAGAGCCAAATTGAAGTCTACCTAACA ACCAAGTAACTTTTTGCTTTTTGGCAACCTTACCTACTGCTGGATTTAGAAATTTTATTGC acreaactraagaaccaagagargccaactrrartraaggaraaaaacgrrgararrar GGTGTAGAATATTACCATCTCTGTTATTTATGTGAAAATGCAGAAAGGAGTGCATGTATC TACGGAGGGGTAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT TACGGAGGGGTAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT 1275 AAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAATG AAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAATG GTAACTGCTCAAGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTA TATACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTCATACCTAAGAATAAA ATATATAAAGATAATGAAACGCTTGACTCAAACACAAGCCAAATTGAAGTCTACCTAACA ACCAAGTAACTTTTTGCTTTTTGCCAACCTTACCTACTGCTGGATTTAGAAATTTTATTGC AAAATGGTATTTTTTTAGTGACATTTCTTGGACTAACAATCTCGCAAGAGGTATTT ACTGAACTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAAACGTTGATATTTAT CCTAAAATATACCCCTTATCAATCGCTTCTTTAAACTCATCTATATAAAATATTTCAT **AATAAAATTATTAATATAAGTTAATGTTTTTAAAAATATATACAATTTTATTCTATTTATA** CCTAAAATATACCCCTTATCAATCGCTTCTTTAAACTCATCTATATAAACATATTTCAT CCTCCTACCTATCTATTCGTAAAAAGATAAAAAAAAATAACTATTGT 1515 1501 961 1095 1081 1141 1261 1321 1381 1455 1441 1575 541 1035 1021 1155 1215 1201 1335 1395 615 601 661 795 855 841 915 901 675 735 721 781 975 8 6 8 6 8 6 8 6 8 & 8 र्घ क्ष ठ 8 6 8 6 8 8 à 원 장 연 8 & 8 & ð 셤 ð 원 8 8 ₹

1741 freareserariccearrirresacasearesresresresresrereraeacaeaaarear 1800 q ρλ GCTTTACCTCCTAATGCTGCAAAATTTTAAATGTTGGATTTTTGTATTTGTCTATTGTAT GCTTTACCTCCTAATGCTGCAAAATTTTAAATGTTGGATTTTTTGTATTTGTATTGTAT TIGATGGGTAATCCCATTTTTCGACAGACATCGTCGTGCCACCTCTAACACCACAAAATCAT Method for detecting target bacterial species in a sample, comprises detecting the presence or amount of bacterial nucleic acid amplified primer derived from bacterial DNA, specific for the target bacterial Detection; bacterial species; animal; food; environment; antibiotic resistance; ds. 1815 AGACAGGAGCTTGTAGCTTAGCAACTATTTATCGTC 1851 Streptococcus pyogenes polynucleotide SEQ ID NO 33 The Sales Claim 6; Page 107-108; 168pp; English. IDII-) IDI INFECTIO DIAGNOSTIC INC. Roy BP 95NZ-00501596. ABA76857 standard; DNA; 1837 Ouellette M, (first entry) 1635

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                                                               CAACTTTTATCTCACGATTTAATATATATATTTTCAGGGCCAAATTATGATAAAA
                                                                                                ACTGAACTTAAGAACCAAGAGGAACTTTATTTAAGGATAAAACGTTGATATTTAT
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           1081 ACTGAACTTAAGAACCAAGAGAGGGAACTTTATTTAAGGATAAAAACGTTGATATTAT
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identification that can be achieved, which reduces the time currently required for the identification of pathogens in the clinical laboratory
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99.2%; Score 1835.4; DB 4; Length 1837;
Best Local Similarity 99.9%; Pred. No. 1.4e-286;
Matches 1836; Conservative 0; Mismatches 1; Indels 0;
                                     Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 U; 0 Other;
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cytostatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42; diagnosis; treatment; superantigen-associated bacterial infection; ds.
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groduct= "Streptococcal pyrogenic exotoxin A (SPE-A)"
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Pred. No. 4.7e-286;
0; Mismatches 3;
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Best Local Similarity 99.8%;
Matches 1834; Conservative
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disrupt contact between the toxin and the HLA-DR receptor, reducing DR1 binding. SPEA42 can be expressed as a recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPEA42 is highly antigenic, inducing protective immunity in a mouse animal model. The attendated superantigen can be used to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSST-1 and SPEA is predicted to provide protective immunity against the majority of bacterial superantigen toxins
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                                                                                                                                                                                                                                                                                                             Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;
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                                                                                                                        1501 ATATATAAAAGATAATGAAACGCTTGACTCAAACACAAGCCAAATTGAAGTCTACCTAACA
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attenuation, mutant, gene; ss.
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CAACTAGATTGACAACTAATTCTCAACAAACGTTAATTTAACAACATTCAAGTAACTCCC 254 New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been aleared so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen sessociated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analyzing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents DNA encoding streptococcal pyrogenic exotoxin A rcargringacagcriarcarcaaraagcriacrirircaaarcaggrcrarccrigaaac TCATGITIGACAGCITATCATCGATAAGCITACTITICGAATCAGGTCTATCAAAC AGGTGCAACATAGATTAGGGCATGGAGATTTACCAGACAACTATGAACGTATATACTCAC egrupernto exotoxin A; ds; superantigen-associated bacterial infection; superantigen toxin; gene; vaccine. Gaps Length 1837; ; 0 Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other; 3; Indels 99.0%; Score 1832.2; DB 7; 99.8%; Pred. No. 4.7e-286; iive 0; Mismatches 3; exotoxin A" tct= "Pyrogenic streptococcal pyrogenic 16cation/Qualifiers 814. 1569 /*tag* a Claim 9; Page 32-34; 50pp; English ŝ Bavari 97US-008B2431. 97MS-00882431 ACA61184 standard; DNA; 1837 (first entry) Best Local Similarity Matches 1834; Conservative Ulrich RG, Olson MA, Similarity WPI; 2003-401542/38 P-PSDB; ABU10088. ULRICH R G. OLSON M A. BAVA/) BAVARI S. Streptococcus sp. JŚ2003009015-A1. DNA encoding 5-JUN-1997; 3-Jun-1997; 11-AUG-2003 09-JAN-2003 75 61 135 195 Query Match Best Local S 15 (ULRI/) (OLSO/) ద 8 6 ઠ 셤

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The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA. This sequence is used in the invention superantigen toxin DNA fragment, useful for preparing treating or preventing bacterial infection. 4; Page 128-129; 141pp; English

Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Gaps Score 1832.2; DB 8; Length 1837; Pred. No. 4.7e-286; 0; Mismatches 3; Indels 0; Query Match Best Local Similarity 99.8%; Matches 1834; Conservative d

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                                                                                                                                                                                                                        SPEa, streptococcus pyrogenic enterotoxin a, gene, mutant, vaccine, de superantigen toxin, MHC, superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                       Streptococcus pyrogenic toxin a L42R mutant, DNA
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                                                                                                                   ACD28901 standard; DNA; 1837
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sequence encodes the L42R (with reference to the mature protein) mutant of SPBa
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                                                                                      98.9%; Score 1830.6; 'DB 8, 99.8%; Pred. No. 8.6e-286; Live 0; Mismatches 4;
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Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; S. pyogenes exotoxin (SPEA) gene. ACA64700 standard; DNA; 1031 BP (first entry) 18-JUN-2003 ACA64700; MAKE KEKEKE KE

tumour 968oclated lipid, anergy, T cell, antigen presenting cell, APC; tumour;cidal immunocyte, antitumour. 30-MAY-2001; 2001US-00870759. 31-MAY-2000; 2000US-0208128P. Streptogoccus pyogenes TERM/) TERMAN S. US2602177551-A1. 28 NOV-2002.

WPI; 2003-361759/34. rerman DS;

P-PSDB; ABU79074

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in I cells and antigen presenting cells.

Disclosure, Page, 167pp, English.

The invention relates to a manmalian cell receptor, useful in the creatment of cancer, which binds to tunnour associated lipids and induces an erray or apoptosis in the T cells and antigen presenting cells (APCS).

Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tunnour associated lipids and induces calluding that atmonticidal immuncyte population in vivo in a manmal to producing (MI) at tunnouricidal immuncyte population in vivo in a manmal of the receptors for immunosypessive fatty acids, ceramides, glycolpids, prophessive fatty acids, ceramides, glycolpids, cells of immunosypessive fatty acids, ceramides, glycolpids, sphingolpids, glycosphingolpids, phosphosphips are alactivated or celetorial atmontant in the treatment of cencer comprising a sphingolpids, glycosphingolpids, phosphosphips are alactivated or celetorial acids, acomposition useful in the treatment of cencer (where an adaptor procein which inhibit treatment of cencer (where an adaptor procein which confident tunnucionally deactivated), a composition useful in the treatment of cencer (comprising a lipid raft conjugated to a superamingen), producing (MI) a tunnucidal immunocyte population are superamingen, to produce a curcinated are inactivated or produce a tunnucidal immunocyte population, and adminisering humanocytes population, and adminisering the tunnucidal immunocyte population, and adminisering the tunnucidal accordated lipids to contact reals, in which aceptors for the tunnucidal activated or produce a tunnucidal activated or produce a tunnucidally activated or produce a tunnucidal accordated lipids to contact reals, in which adaptor produces, and adminisering the tunnucidally activated or produce a tunnucidally activated or produce a tunnucidally activated or produce a tunnucidally activated or produce a tunnucidally activated or produce a tunnucidally activated or produce a tunnucidally activated or produce a tunnucidal and an ammal ly adminisering a selector to manumal ly adminisering

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                                                                                                               Length 1031;
                                                                Sequence 1031 BP; 381 A; 146 C; 162 G; 342 T; 0 U; 0 Other;
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    the US patnet office website at
"segdata.uspto.gov/seguence.html?DocID=20020177551"
                                                                                                               Score 892.8; DB 7;
Pred. No. 7.2e-135;
0; Mismatches 37;
                                                                                                             DB 7;
                                                                                                                  48.2%;
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Matches 993; Conservative
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Species specific, genus specific, family specific, probe, detection, identification, algal, archaeal, bacterial, fungal, parasitical, microorganism, diagnosis, translation elongation factor Tu; toxin, translation elongation, factor G, RecA recombinase, resistance, catalytic subunit of proton-translocating ATPase, antimicrobial, vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified nucleotide sequence SEQ ID NO:993.
1709 IGCIGCAAATITIAAAIGITGGATITITGIAIT
                                                                                                                                                                                 1014 CATTTTCGACAGACATC 1031
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Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.

Ouellette M;

Menard C,

Huletsky A,

Boissinot M,

Disclosure; Page 957; 1580pp; English

The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parastical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, bacteria, fungal and parasites, for universal detection and for specific and ubiquitous parasitical species, genus, family and group. A mucleic acid (I) obtained using the method of the invention of an algal, archaeal, bacterial, fungal and using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, backing and Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria agnorrhoace and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved, AAH00010 to AAH002304

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superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial; SPEb.

(pos:298. .306,aa:Ile-Gly) (pos:634. .642,aa:Thr-Gln) (pos:1162. .1170,aa:Ser-Gln) (pos:1228. .1236,aa:Gly-Gly)

L42R/SPED

1. 1419 //trage a SPEa L /transl_except= /transl_except= /transl_except= /transl_except= /transl_except=

970S-00882431. 98US-00144776.

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ULRI/) ULRICH 25-JUN-1997; 01-SEP-1998;

Ulrich RG

26-NOV-2001; 2001U\$-00002784

US2003036644-A1

20-FEB-2003.

Location/Qualifiers

Key

Streptococcus sp. Synthetic.

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                                                                                       181 ACTCACGAGAATGTGAATCTGTTGATCAACTTTTATCTCACGATTTAATATATGTT
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                                              Score 754.4; DB 4; Length 756; Pred. No. 1.4e-112; 0; Mismatches 1; Indels 0
                             Sequence 756 BP; 297 A; 110 C; 118 G; 231 T; 0 U; 0 Other;
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represent nucleotide sequences and prime exemplification of the present invention
                                                40.8%;
Local Similarity 99.9%;
hes 755; Conservative
                                                Query Match
Best Local S:
Matches 755
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New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

WPI; 2003-492125/46. P-PSDB; ABU62335.

Claim 6; Page 39-40; 68pp; English

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The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MRC class I for cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, superantigen toxin peptide, diagnosing superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an arting/ameliorating a superantigen-associated bacterial infection, treating/ameliorating a superantigen-associated bacterial infection, an antimodated from individuals immunised with one or more altered TST-1. Superantigen toxin and an antibody which recognises altered TST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating a preventing bacterial infection. The present sequence encodes the SPEB L42R/SPEB C47S mutant fusion protein
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SPEa L42R/SPEb C47S mutant fusion protein, DNA.

(first entry)

27-AUG-2003

ACD28908

ACD28908 standard; DNA; 1419

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AAGTAACTTTTTGCTTTTGCCAACCTTACCTACTGCTGGATTTAGAAATTTTATTGCAAT 1637
                                                                                                                                                                           Sequence 1419 BP; 497 A; 266
                                      WPI; 2003-492125/46
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                                                                                                       GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAAATGGTA
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                       184 GAACTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAAAACATTGATATTTATGGT
                                                                       1218 GGAGGGGTAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTTAAA
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The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T call antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA)-SpeB fusion DNA. This sequence is used in the invention
                                                                                                                                                                                                                                            composition
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Best Local Similarity 94.2%; Pred. No. 7e-97;
Matches 682; Conservative 0; Mismatches 42; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 255 G; 401 T; 0 U; 0 Other;
                                                                                                                                                                                                                                            New superantigen toxin DNA fragment, useful for preparing for treating or preventing bacterial infection.
MEDICAL RES INST INFECTIOUS DISEASES
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The invention relates to a mammalian cell receptor, useful in the anergment of cancer, which binds to tumour associated lipids and induces anergy or appropsis in the T cells and antigato presenting cells (ARCS).

Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycophingolipids, ghosphosphingolipids, ghosphosphingolipids, ghosphosphingolipids, gangliosides, slalylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which useful in the treatment of cancer (where an adaptor protein which intitionally deactivated), a composition useful in the treatment of cancer (where an adaptor protein which cancer (comprising a lipid raft conjugated to a superantigen) producing (M2) a tumour icidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the host, producing a tumour associated lipids are inactivated or deleted to produce a cumouricidally activated population, and administering the tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated a tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering a tumour cidal I produce a lipids are inactivated or deleted to produ
A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superantigen, ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus/Streptococcus erythrogenic toxin gene.
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Streptococcus sp.
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contact T calls, in which adaptor proteins, which inhibit T cell
activated to produce a tumouricidal population of T cells, and
activated to produce a tumouricidal population of T cells, and
administering the tumouricidally activated T cells to the host, or
allowing a superantigen-lipid raft to contact T cells ex vivo, and
administering the tumouricidally activated T cells to the host, treating
administering the tumouricidally activated T cells to the host, treating
(M5) cancer in a mammal (by administering a lipid binding molecule which
binds immunosuppressive tumour associated lipids in vivo), producing (M6)
a tumour associated antigen to contact immunocytes in which adaptor.

CC tumour associated antigen to contact immunocytes in which adaptor.

CC tumour associated or functionally deactivated) and producing (M7) a

tumouricidal T cell population ex vivo in a mammal comprising allowing a

cumouricidal T cell population ex vivo in a mammal comprising allowing a

tumours. Bacterial superantigens are co-administered or administered as

tumours. Bacterial superantigens are co-administered or administered as

tumours and on a fusion construct with a superantigen. Note: The

sequence encodes an anti-tumour protein which is co-administered

c incorporated into a fusion construct with a superantigen. Note: The

sequence date for this patent did not form part of the printed

specification, but was obtained in electronic format from the US patnet

coffice website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
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  population ex vivo in a mammal) by allowing a tumour associated lipids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%; Score 278; DB 7; Length 1497; larity 99.7%; Pred. No. 6.5e-36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1497 BP; 584 A; 247 C; 246 G; 420 T; 0 U; 0 Other;
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/*tag= a
//product= "Staphylococcal enterotoxin
247. .327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATATATATTTTTTTTATGAGGGTGACCCTGTTACTCACGAGAATGTGAAATCTGTTG 1032
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/*tag= b
328. .1041
/*tag= c //abel= Mature_Staphylococcal_enterotoxin_B //note= "Also includes the ATG_start codon" //transl_except= (pos:9712. .774, aa:Tyt) //transl_except= (pos:901. .903, aa:Gln) //transl_except= (pos:904. .909, aa:Asn) //transl_except= (pos:1012. .1014, aa:Leu)
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Pred. No. 8.1e-21;
0; Mismatches 408; Indels
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Best Local Similarity 54.5%;
Matches 552; Conservative (
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P-PSDB; AAY70104.
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